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OM protein - protein search, using sw model

Run on: February 26, 2002, 08:04:11 ; Search time 23.85 Seconds  
(without alignments)  
15.529 Million cell updates/sec

Title: US-09-658-315-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_1101.\*  
1: /SID88/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
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11: /SID88/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
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13: /SID88/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID88/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID88/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID88/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID88/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	5	17	AA95670 Angiotensin II fra
2	26	100.0	5	19	AAW64736 Angiotensin II pep
3	26	100.0	5	19	AAW65605 Angiotensin II ana
4	26	100.0	5	19	AAW71118 Peptide AII(1-5) u
5	26	100.0	5	20	AAW49594 Angiotensin analog
6	26	100.0	5	20	AAW33909 Angiotensin II ana
7	26	100.0	5	20	AAW30547 Amino acid sequenc
8	26	100.0	5	20	AAW30591 Amino acid sequenc
9	26	100.0	5	20	AAW32722 Angiotensin II ana
10	26	100.0	5	20	AAW33776 Angiotensin II (AI
11	26	100.0	5	20	AAW15353 Angiotensin II (AI

12	26	100.0	5	20	AAW15313 Angiotensin II (AI
13	26	100.0	5	21	AAW27409 Angiotensin II ana
14	26	100.0	5	21	AAW28107 Angiotensin II ana
15	26	100.0	5	21	AAW84568 Amino acid sequenc
16	26	100.0	5	21	AAW84132 Peptide comprising
17	26	100.0	5	21	AAW77045 Angiotensin II (AI
18	26	100.0	5	21	AAW57409 Angiotensin peptid
19	26	100.0	5	22	AAW02996 Human angiotensin
20	26	100.0	5	22	AAW03159 Human angiotensin
21	26	100.0	5	22	AAW60413 C-terminally trunc
22	26	100.0	6	17	AAW95669 Angiotensin II fra
23	26	100.0	6	19	AAW65604 Angiotensin II ana
24	26	100.0	6	19	AAW64735 Angiotensin II pep
25	26	100.0	6	19	AAW71117 Peptide AII(1-6) u
26	26	100.0	6	20	AAW49593 Angiotensin analog
27	26	100.0	6	20	AAW33908 Angiotensin II ana
28	26	100.0	6	20	AAW30546 Amino acid sequenc
29	26	100.0	6	20	AAW30590 Amino acid sequenc
30	26	100.0	6	20	AAW32721 Angiotensin II ana
31	26	100.0	6	20	AAW33775 Angiotensin II (AI
32	26	100.0	6	20	AAW15352 Angiotensin II (AI
33	26	100.0	6	20	AAW15312 Angiotensin II (AI
34	26	100.0	6	21	AAW27408 Angiotensin II ana
35	26	100.0	6	21	AAW28106 Peptide comprising
36	26	100.0	6	21	AAW84131 Angiotensin II (AI
37	26	100.0	6	21	AAW77044 Angiotensin peptid
38	26	100.0	6	21	AAW57408 Human angiotensin
39	26	100.0	6	22	AAW02995 Angiotensin II fra
40	26	100.0	6	22	AAW03158 Angiotensin II ana
41	26	100.0	7	17	AAW95665 Angiotensin II fra
42	26	100.0	7	19	AAW65600 Angiotensin II ana
43	26	100.0	7	19	AAW64731 Angiotensin II pep
44	26	100.0	7	19	AAW71113 Peptide AII(1-7) u
45	26	100.0	7	20	AAW49589 Angiotensin analog

ALIGNMENTS

RESULT 1  
AA95670 ID AAR95670 standard; peptide; 5 AA.  
XX AAR95670;  
DT 09-JAN-1997 (first entry)  
XX  
DE Angiotensin II fragment AII(1-5).

XX Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;  
KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;  
KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.

OS Synthetic.

XX WO9614858-A1.

PD 23-MAY-1996.

XX 14-NOV-1995; 95WO-US14764.

XX 06-JUN-1995; 95US-0465775.

PR 14-NOV-1994; 94US-0337781.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers K;

DR WPI; 1996-259561/26.

XX Accelerating wound healing by application of angiotensin II  
PT fragments - are effective at very low concn. and do not cause  
PT hypertension

XX Disclosure; Page 4; 46pp; English.

XX AAR95663-R95672 represent fragments of angiotensin II (AT2). AT2 (see

CC AAR95662) is an octapeptide present in humans and other species. AT2 is

CC one of the most potent vasoconstrictors known, causing constriction of

CC the arterioles. The formation of angiotensin is initiated by the action

CC of renin on angiotensinogen. The substance formed is a decapeptide

CC called angiotensin I which is converted by the enzyme angiotensinase (by

CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release

CC of extracellular matrices involved in wound repair. These fragments can

CC be used in a compound for accelerating wound healing. The compounds are

CC administered as matricial or micellar solutions formulated with a

CC carrier or diluent, alternatively the compound is applied in conjuncture

CC with a wound dressing. The carrier used in the composition is

CC preferably carboxymethylcellulose, crystalloids, viscoelastics, or poly

CC glycols. By using fragments of this sequence (or analogues of it),

CC growth as well as healing of tissues is improved, such as in cases of

CC wounds on the skin (e.g. ulcers, burns, periodontal disease, cuts) or

CC intraperitoneal surgical wounds. The compounds containing the AT2

CC fragments are less hypertensive than full length AT2, and are also

CC effective at much lower (nanomolar) concentrations than full length AT2.

XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 |||||  
 Db 1 drvyl 5

RESULT 2  
 AAW64736  
 ID AAW64736 standard; peptide; 5 AA.

XX AAW64736;

XX 02-NOV-1998 (first entry)

XX Angiotensin II peptide #8.

XX Proliferation; mesenchymal stem cell; lineage-specific cell;  
 KW haematopoietic; cell culture; transplantation; treatment; malignant;  
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.

XX Synthetic.

OS Homo sapiens.

XX WO9832457-A2.

XX 30-JUL-1998.

XX 26-JAN-1998; 98WO-US01552.

XX 23-JAN-1998; 98US-0066593.

PR 28-JAN-1997; 97US-0036507.

PR 08-MAY-1997; 97US-0046859.

PR 28-OCT-1997; 97US-0063684.

PR 31-OCT-1997; 97US-0063910.

PR 18-NOV-1997; 97US-0065612.

PR 26-NOV-1997; 97US-0066593.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

XX WPI; 1998-437044/37.

XX Promoting haematopoietic and mesenchymal cell proliferation and

PT differentiation - by contacting the cells with angiotensinogen,  
 PT angiotensin I or II, or analogues or fragments of these

XX Claim 7; Page 14; 114pp; English.

XX AAW64728-R64763 are peptides used in a novel method for accelerating the

CC proliferation of mesenchymal stem cells (MSCs), haematopoietic

CC lineage-specific cells or mesenchymal lineage-specific cells. The method

CC involves contacting the cells with an active agent comprising a sequence

CC consisting of at least three contiguous amino acids of groups R1-R8 in

CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together

CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,  
 CC Ala, Leu, norLeu, Ile, Gly, Pro, Aib, Acpc (1-aminocyclopentane  
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoSer or  
 CC azArg, R5 = Ile, Ala, Leu, norLeu, Val or Gly; R6 = His, Arg or  
 CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are  
 CC not defined in the specification, the peptide bond between Ra and Rb is

CC labile to aminopeptidase A cleavage excluding sequences including R4 as a

CC terminal Tyr group. A second active agent comprising a sequence

CC consisting of at least three contiguous amino acids of groups R2-R8 in

CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,  
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also  
 CC described. The inventions are particularly useful in cell culture

CC mediums. These cells may be used in transplantation techniques for

CC treatment of malignant or inherited diseases. The formulae represent

CC analogues of angiotensinogen, angiotensin I (AI), angiotensin II (AII),  
 CC or AII AT2 type 2 receptor agonists.

SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 |||||  
 Db 1 drvyl 5

RESULT 3  
 AAW65605

ID AAW65605 standard; peptide; 5 AA.

XX AAW65605;

XX 09-NOV-1998 (first entry)

XX Angiotensin II analogue, AII(1-5).

XX angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;  
 KW wound healing.

OS Synthetic.

OS Homo sapiens.

XX WO9826795-A1.

XX 25-JUN-1998.

XX 16-DEC-1997; 97WO-US23461.

XX 15-DEC-1997; 97US-0990664.

XX 16-DEC-1996; 96US-0028310.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega GS, Rodgers KE;

XX WPI; 1998-362518/31.

XX Promoting incorporation of skin graft onto underlying tissue -

XX comprises pre-treating graft with angiotensin II, or analogue or

PT peptide fragment

PS Disclosure; Page 6; 82pp; English.

XX The invention relates to the use of angiotensin II (AII), AII analogues, AII fragments and AII fragment analogues for promoting incorporation of a skin graft into underlying tissue of a mammal. The peptides are effective in accelerating the growth or healing of skin grafts and in accelerating re-epithelialisation and tissue repair, even at very low concentrations. They can significantly accelerate the rate of healing at nanomolar levels in vivo. AII accelerates wound repair by increased neovascularisation, growth factor release, re-epithelialisation, extracellular matrix production and increased flow of blood and nutrients to the injured tissue. Use of the above peptides other than AII itself (an extremely potent vasoconstrictor) may avoid the side-effects of AII, such as increase in blood pressure and thirst. The present sequence represents an angiotensin II fragment.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
Db 1 drvyi 5

RESULT 4

AAW71118  
ID AAW71118 standard; peptide; 5 AA.

XX AAW71118;

DT 27-OCT-1998 (first entry)

DE Peptide AII(1-5) used to accelerate thermal wound healing.

XX Angiotensin; AII; acceleration; thermal wound healing; human;  
KW growth factor release; neovascularisation; re-epithelialisation;  
KW extracellular matrix production.

XX Synthetic.

XX WO9833813-A2.

XX 06-AUG-1998.

XX 04-FEB-1998; 98WO-US02049.

XX 04-FEB-1997; 97US-0037166.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Dizerega G, Rodgers KE;

DR WPI; 1998-437391/37.

XX Methods for accelerating thermal wound healing in humans - using  
PT angiotensinogen II and AII analogues

PS Claim 3; Page 9; 58pp; English.

XX AAW71110-27 represent peptide used in the method of the invention. The  
CC Specification describes a method of accelerating thermal wound healing  
CC in humans. The method comprises applying to the thermally injured tissue  
CC an amount of at least one active agent which comprises the peptides  
CC AAW71115-27. The method can be used to promote the healing of thermal  
CC wounds by accelerating growth factor release, neovascularisation,  
CC re-epithelialisation and extracellular matrix production. The sequences  
CC are analogues of the angiotensin or angiotensinogen family of proteins.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
| | | | |  
Db 1 drvyi 5

RESULT 5

AAAY49594

ID AAY49594 standard; peptide; 5 AA.

XX AAY49594;

XX 13-JAN-2000 (first entry)

XX Angiotensin analogue peptide SEQ ID NO:9.

XX Angiotensin I; angiotensin II; angiotensinogen; AI; AII; Infection;

KW receptor agonist; septic shock; peritonitis; bacteraemia; endotoxaemia.

XX Synthetic.

XX WO9952540-A1.

XX 21-OCT-1999.

XX 07-APR-1999; 99WO-US07654.

XX 09-APR-1998; 98US-0081262.

XX 12-JUN-1998; 98US-0089024.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers KE, Dizerega G;

XX WPI; 1999-620285/53.

XX Treating or preventing infections in mammals using peptides derived  
PT from angiotensin or angiotensin receptor agonists

PS Claim 2; Page 10; 91pp; English.

XX The present invention describes a method for treating or preventing  
CC infections in mammals by administering peptides (A) that are fragments  
CC or analogues (or their fragments) of angiotensinogen, angiotensins I or  
CC II, or angiotensin II AT<sub>2</sub>-type receptor agonists. (A) contain at least  
CC 3 consecutive amino acids (aa) from the sequence (S1):  
CC RI-R2-R3-R4-R5-R6-R7-R8 (S1); where RI and R2 together = X-Ra-Rb-;  
CC X = hydrogen or 1-3 aa; Ra = Asp, Glu, Asn, Acpc (1-aminocyclopentane  
CC carboxylic acid), Ala, dimethylglycine, Pro, betaine, Glu(NH<sub>2</sub>), Gly,  
CC Asp(NH<sub>2</sub>) or succinyl; Rb = Arg, Lys, Ala, ornithine, acetyl-Ser,  
CC sarcosine, D-Arg or D-Lys; R3 = Val, Ala, Leu, norleucine (Nle), Lys,  
CC Ile, Gly, Pro, Aib (2-aminoisobutyric acid), Acpc or Tyr; R4 = Tyr  
CC (optionally phosphorylated), Thr, Ser, homoserine, Pro, Ala or azo-Tyr;  
CC R5 = Ile, Ala, Leu, Nle, Val or Gly; R6 = His, Arg or 6-amino-Phe;  
CC R7 = Pro or Ala; R8 = Phe, 4-bromo-Phe, Ile or Tyr; proviso =  
CC sequences having R4 as a terminal Tyr residue are excluded. The method  
CC is particularly used in cases of bacterial infection (e.g. septic shock,  
CC peritonitis, bacteraemia or endotoxaemia) but also against viral and  
CC parasitic infections. AAY49596 to AAY49623 represent specifically  
CC claimed examples of (A).

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 1 drvyi 5

## RESULT 6

AAAY33909  
ID AAY33909 standard; peptide; 5 AA.

XX  
AC AAY33909;

XX  
DT 29-NOV-1999 (first entry)

XX  
DE Angiotensin II analogue AII(1-5).

XX  
KW embryonic stem cell; ES; angiotensin; totipotent cell;  
KW gene therapy; replacement therapy; angiotensin II; AII;  
KW analogue.

XX  
OS Homo sapiens.

XX  
PN W09942122-A1.

XX  
PD 26-AUG-1999.

XX  
PF 16-FEB-1999; 99WO-US03243.

XX  
PR 19-FEB-1998; 98US-0075179.

XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX  
PI Dizerega G, Rodgers KE;

XX  
DR WPI; 1999-527419/44.

XX  
PT Promoting embryonal cell proliferation, using angiotensinogen and  
PT angiotensin peptides, analogs or fragments

XX  
PS Claim 2; Page 8; 76pp; English.

XX  
CC This is the amino acid sequence of the Angiotensin II analogue,  
CC AII(1-5). The formation of Angiotensin II (AII) is initiated by the  
CC action of renin on the plasma substrate angiotensinogen.

XX  
CC This results in Angiotensin I (AI) which then converted to AII by the  
CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
CC residues from AI (AAY42372).

XX  
CC Angiotensinogen, Angiotensin I (AI), AI analogs, AI fragments and  
CC analogs, Angiotensin II (AII), AII analogs, AII fragments or analogs,  
CC or AII AT2 type 2 receptor agonists can rapidly provide a large  
CC population of ESCs (Embryonic Stem Cell) for use in replacement  
CC therapy. Similarly, methods that increase in vivo proliferation of  
CC ESCs will enhance the utility of replacement therapy by rapidly  
CC increasing local concentration of the stem cells and their progeny at  
CC the site of therapy.

XX  
CC The method also increases the potential utility of ESCs as vehicles  
CC for gene therapy in certain disorders by more efficiently providing  
CC a large number of such cells for transfection, and also by providing a  
CC more efficient means to rapidly expand transfect ESCs.

XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 1 drvyi 5

## RESULT 7

AAAY30547  
ID AAY30547 standard; peptide; 5 AA.

XX  
AC AAY30547;

XX  
DT 18-NOV-1999 (first entry)

XX  
DE Amino acid sequence of angiotensin II fragment AII1-5.

XX  
KW Angiotensin; analogue; tissue equivalent; cell proliferation.

XX  
OS Synthetic.

XX  
PN W09946285-A2.

XX  
PD 16-SEP-1999.

XX  
PF 11-MAR-1999; 99WO-US05261.

XX  
PR 11-MAR-1998; 98US-0077499.

XX  
PR 12-JUN-1998; 98US-0089064.

XX  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX  
PI Rodgers KE, Dizerega G;

XX  
DR WPI; 1999-551360/46.

XX  
PT An improved method for producing a tissue equivalent with angiotensin I  
PT and II derived active agents -

XX  
PS Claim 2; Page 56; 83pp; English.

XX  
CC AAY30539-80 represent angiotensin I (AI) and angiotensin (II), AII  
CC fragments and AII analogues. The peptides are used in the method  
CC of the invention. The specification describes an improved method  
CC for producing a tissue equivalent. The method comprises contacting  
CC the tissue equivalent with angiotensin I and II derived active  
CC agents. The methods are used for production and culture of tissue  
CC equivalents (three-dimensional cell and tissue culture systems),  
CC chosen from skin, dermis, bone, bone marrow, pancreas, heart valve,  
CC vascular graft, cartilage, ligament, collagen lattice, liver and  
CC kidney tissue equivalents. The methods and tissue culture systems  
CC are used for the long-term proliferation of cells and tissues  
CC in an in vitro environment that more closely approximates that found  
CC in vivo.

XX  
SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 1 drvyi 5

## RESULT 8

AAAY30591  
ID AAY30591 standard; peptide; 5 AA.

XX  
AC AAY30591;

XX  
DT 18-NOV-1999 (first entry)

XX  
DE Amino acid sequence of an angiotensin II (AII) fragment AII1-5.

XX  
KW Angiotensin; analogue; radiation mitigation; tissue damage;

KW radiation therapy; bone marrow transplantation;

KW megakaryocyte production; platelet production; cancer therapy;

KW gene therapy; hematopoietic disorder.  
 XX Synthetic.  
 OS WO9945945-A1.  
 PN 16-SEP-1999.  
 XX 08-MAR-1999; 99WO-US05194.  
 PD 10-MAR-1998; 98US-0077382.  
 XX 09-APR-1998; 98US-0081262.  
 PR 30-APR-1998; 98US-0083670.  
 PR 19-JUN-1998; 98US-0090096.  
 PR 22-JUN-1998; 98US-0090216.  
 PR 11-SEP-1998; 98US-0099957.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 PA (RODG/) RODGERS K E.  
 PA (DIZE/) DIZEREGA G.  
 XX Rodgers KE, Dizerega G;  
 PI WPI; 1999-551209/46.  
 XX Use of angiotensin and angiotensin type peptides, for mitigating  
 PT radiation induced tissue damage, improving bone marrow transplantation  
 PT and promoting megakaryocyte and platelet production -  
 XX Claim 2; Page 89; 116pp; English.  
 PS AAY30583-Y30620 represent angiotensin I (AI) and angiotensin (II), AII  
 XX fragments and AII analogues. The peptides are used in the method  
 CC of the invention. The specification describes a method for mitigating  
 CC radiation induced tissue damage, improving the effectiveness of  
 CC radiation therapy, to support bone marrow transplantation, and  
 CC promoting megakaryocyte production and mobilization and platelet  
 CC production. The method comprises administration of the present peptides.  
 CC The methods can be used to mitigate radiation induced tissue damage, to  
 CC improve the effectiveness of radiation therapy, to support bone marrow  
 CC transplantation, and to promote megakaryocyte production and  
 CC mobilization and platelet production. They are used particularly in  
 CC cancer therapy. They can also be used to provide megakaryocytes as  
 CC vehicles for gene therapy in hematopoietic disorders, by providing a  
 CC more efficient means to rapidly expand transduced megakaryocytes.  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYI 5  
 Db | | | | |  
 1 drvyi 5  
 RESULT 9  
 AAY32722  
 ID AAY32722 standard; peptide; 5 AA.  
 XX AAY32722;  
 AC  
 DT 09-NOV-1999 (first entry)  
 XX Angiotensin II analogue AII(1-5).  
 DE Angiotensin II; AII; hepatocyte; proliferation; mitogenesis;  
 KW chemotaxis; growth factor; liver regeneration; cirrhosis;  
 KW hepatocarcinoma; hepatectomy; transplantation.  
 XX Synthetic.  
 OS

OS Homo sapiens.  
 XX WO9939743-A2.  
 PN 12-AUG-1999.  
 PD 08-FEB-1999; 99WO-US02618.  
 PF 13-NOV-1998; 98US-0108412.  
 XX 09-FEB-1998; 98US-0074104.  
 PR (DIZE/) DIZEREGA G.  
 XX (RODG/) RODGERS K E.  
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1999-508461/42.  
 DR Hepatic cell proliferation with angiotensin I and II derived active  
 XX agents, useful for regeneration of liver after resection  
 PT Claim 2; Page 9; 66pp; English.  
 PS Peptides AAY32715-Y32749 are angiotensin II (AII) analogues. The  
 XX peptides are derived from the AII peptide (AAY32750). AII increases  
 CC mitogenesis and chemotaxis in cultured cells, and also increases the  
 CC release of growth factors and extracellular matrices. AII has also been  
 CC shown to increase the proliferation of certain cell types. The AII  
 CC analogue peptides can be used as the active agent in a method for  
 CC promoting hepatic cell proliferation and differentiation. The method  
 CC involves contacting the hepatic cells with an amount effective enough to  
 CC promote proliferation of any of the peptides. This method is useful in  
 CC liver regeneration following resection of hepatocarcinomas, hepatitis  
 CC infection, cirrhosis of the liver, partial hepatectomy, fulminant hepatic  
 CC failure, hepatocyte transplantation, liver transplantation and other  
 CC hepatic disorders where rapid regeneration of the liver is desirable. The  
 CC methods are also useful in rapidly providing a large population of  
 CC hepatic cells for use in cell therapy and for providing a large  
 CC population of transduced hepatic cells for use in gene therapy.  
 XX Sequence 5 AA;  
 SQ Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYI 5  
 Db | | | | |  
 1 drvyi 5  
 RESULT 10  
 AAY33776  
 ID AAY33776 standard; peptide; 5 AA.  
 XX AAY33776;  
 AC  
 DT 09-NOV-1999 (first entry)  
 XX Angiotensin II (AII) octapeptide fragment AII(1-5).  
 DE Angiotensin II; wound healing; mitogenesis; chemotaxis; growth factor;  
 KW neuronal cell proliferation; differentiation; Alzheimer's disease;  
 KW Parkinson's disease; neuron replacement therapy.  
 XX Homo sapiens.  
 OS  
 XX WO9942123-A1.  
 PN 26-AUG-1999.  
 XX

PF 19-FEB-1999; 99WO-US03772.  
 PR 19-FEB-1998; 98US-0075232.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1999-527420/44.  
 DR Promoting neuronal cell proliferation and differentiation  
 XX Claim 2; Page 10; 62pp; English.

XX Sequences AAY33769-Y33802 are fragments or analogues of the angiotensin  
 CC II (AII) octapeptide (AAY33768) and they have AT2 agonist activity. The  
 CC application of angiotensin to wound tissue significantly increases the  
 CC rate of wound healing. AII is known to increase mitogenesis and  
 CC chemotaxis in cultured cells, and also increases their release of growth  
 CC factors and extracellular matrices, implicating it in cell growth and  
 CC differentiation. AT2 receptors are receptors for AII and are thought to  
 CC be involved in the mediation of the cell differentiation effects of AII.  
 CC Peptides AAY33768-Y33802 are used in a method for promoting neuronal  
 CC cell proliferation or differentiation. This method is useful in the  
 CC treatment of Alzheimer's and Parkinson's diseases by neuron replacement  
 CC therapy.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 DRVYI 5  
 |||||  
 Db 1 drvyi 5

RESULT 11  
 AAY15353  
 ID AAY15353 standard; peptide; 5 AA.  
 AC AAY15353;  
 XX 09-NOV-1999 (first entry)  
 DT Angiotensin II (AII) analogue, AII(1-5).  
 DE burst forming units-erythroid; BFU-E; erythropoiesis; angiotensin;  
 XX AII; analogue; chronic renal failure; cancer; bone marrow.

XX Synthetic.  
 OS Homo sapiens.  
 OS WO9940106-A2.  
 PN 12-AUG-1999.  
 PD 08-FEB-1999; 99WO-US02648.  
 PF 09-DEC-1998; 98US-0111535.  
 PR 09-FEB-1998; 98US-0074106.  
 XX (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1999-508486/42.  
 DR Promoting erythropoiesis with angiotensin I and II derived active  
 XX agents, useful for treatment of, e.g. congenital or acquired  
 PT aplastic or hypoplastic anemia

XX Claim 2; Page 10; 76pp; English.

XX This sequence is an angiotensin II (AII) analogue. Similar sequences  
 CC also based on the AII peptide have been tested against each other, AII  
 CC and a negative control. These active agents have been shown to affect  
 CC the levels of BFU-E (burst forming units-erythroid) in culture.  
 CC The active agents (AAY15348, AAY15359, AAY15372, AAY15379, and AAY15380)  
 CC augment erythropoiesis by potentiating erythropoietin-induced  
 CC differentiation. Increasing the rate of erythropoiesis improves clinical  
 CC benefits for the treatment of congenital or acquired aplastic or  
 CC hypoplastic anemia associated with chronic renal failure, end-stage renal  
 CC disease, renal transplantation, cancer, AIDS, chemotherapy, radiotherapy,  
 CC bone marrow transplantation and chronic diseases.  
 CC The active agents permit the use of smaller doses of erythropoietin  
 CC therefore decreasing treatment costs.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 DRVYI 5  
 |||||  
 Db 1 drvyi 5

RESULT 12  
 AAY15313  
 ID AAY15313 standard; peptide; 5 AA.  
 XX AAY15313;  
 XX 09-NOV-1999 (first entry)  
 DT Angiotensin II (AII) analogue, AII(1-5).  
 DE angiotensin; angiotensin II; AII; wound healing; scarring;  
 KW tissue repair; agonist; analogue.  
 XX Synthetic.  
 OS Homo sapiens.  
 OS WO9940107-A2.  
 PN 12-AUG-1999.  
 PD 08-FEB-1999; 99WO-US02725.  
 PF 09-FEB-1998; 98US-0074105.  
 PR (UYSC-) UNIV SOUTHERN CALIFORNIA.  
 XX Dizerega G, Rodgers KE;  
 PI WPI; 1999-508487/42.

XX Epithelial stem cell and keratinocyte proliferation with angiotensin  
 PT I and II derived active agents, useful for treatment of skin wounds  
 XX Claim 2; Page 10; 70pp; English.  
 XX This is the amino acid sequence of an Angiotensin II analogue. This and  
 CC other similar analogues (AAY15306 to AAY15316 and AAY15321 to AAY15337)  
 CC can be used to promote the proliferation of epithelial stem cells and  
 CC Keratinocytes leading to a more rapid and efficient cellular response to  
 CC stratified epithelial injury. The angiotensin analogues are derived from  
 CC an octapeptide present in humans and other species which has the  
 CC sequence of Asp-Arg-Val-Tyr-Ile-His-Pro-Phe (AAY15342) and is known as  
 CC angiotensin II (AII). This is formed by the action of renin on the  
 CC plasma substrate angiotensinogen, the product of this reaction is a

CC decapeptide called angiotensin I (AI) which is converted to AII by the  
 CC converting enzyme angiotensinase which removes the C-terminal His-Leu  
 CC residues from AI (AAI5339).

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 1 drvyi 5

RESULT 13

AAB27409  
 ID AAB27409 standard; Peptide; 5 AA.

XX AAB27409;

DT 23-JAN-2001 (first entry)

DE Angiotensin II analog AII(1-5).

XX Angiotensinogen; AII; AII; myocyte proliferation; myocardial injury;  
 KW cardiomyopathies; inflammation; infection; sepsis; ischemia;  
 KW heart valve disease; myocarditis; angiotensin.

XX Synthetic.

XX WO200053211-A2.

PD 14-SEP-2000.

PF 09-MAR-2000; 2000WO-US06198.

XX 09-MAR-1999; 99US-0123678.

PR 31-AUG-1999; 99US-0151874.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers K, Dizerega G;

XX WPI; 2000-611400/58.

XX Promoting myocyte proliferation and myocardial tissue repair by  
 PT contacting myocytes with angiotensinogen or angiotensin I or II, useful  
 PT for treating heart attacks, cardiomyopathies, inflammation and  
 PT infection -

XX Claim 2; Page 10; 55pp; English.

XX The present invention relates to a method of promoting myocyte  
 CC proliferation or differentiation by contacting myocytes with an active  
 CC agent containing angiotensinogen, angiotensin I and II (AI, AII), and  
 CC angiotensin analogs. The present sequence is an angiotensin II analog  
 CC of the invention. The active agents of the invention may be useful for  
 CC promoting myocardial tissue repair following myocardial injury and for  
 CC treating heart failure in a mammal. Administration to accelerate in  
 CC vivo myocyte proliferation and/or to treat myocardial injuries can be  
 CC used to treat cardiomyopathies, inflammation, infection, sepsis,  
 CC ischemia, heart valve disease, myocarditis, inflammation, myocardial  
 CC ischemia and infarction and for improving cardiac output by increasing  
 CC stroke volume.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 1 drvyi 5

RESULT 14

AAB28107  
 ID AAB28107 standard; Peptide; 5 AA.

XX AAB28107;

DT 26-JAN-2001 (first entry)

DE Angiotensin II analogue SEQ ID NO: 9.

XX Wound; scar formation; healing; adhesion formation; AII;  
 KW angiotensin II analogue; scar treatment.

XX Synthetic.

XX WO200056345-A2.

PD 28-SEP-2000.

PF 22-MAR-2000; 2000WO-US07669.

XX 23-MAR-1999; 99US-0125707.

PR 16-JUN-1999; 99US-0139541.

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX Rodgers K, Dizerega G;

XX WPI; 2000-587607/55.

XX Limiting scar or adhesion formation comprises administering at least  
 PT one active agent comprising a peptide -

XX Claim 2; Page 10; 54pp; English.

XX The present invention is concerned with peptide analogues of angiotensin  
 CC II (AII) which can be used to limit scar and adhesion formation. The  
 CC application of AII to wound tissue results in a rapid increase in the  
 CC rate of wound healing and causes the proliferation of certain cells, such  
 CC as epithelial cells and keratinocytes. Analogues of the protein have been  
 CC shown to reduce scar formation, and can be used not only to limit new  
 CC scar formation but also to therapeutically treat existing scars. The  
 CC wound types include lacerations, burns, punctures, trauma, ulcers,  
 CC periodontal conditions, laparotomy and incisional wounds, revision of  
 CC hypertrophic scars, genetic hypertrophic scars, keloid scars,  
 CC contractures after burns and cosmetic surgical procedures.

XX Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 Db 1 drvyi 5

RESULT 15

AAI84568  
 ID AAY84568 standard; Peptide; 5 AA.

XX AAY84568;

XX 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of angiotensin I conversion product Ang(1-5).  
 XX Human; angiotensin converting enzyme-2; ACE-2; angiotensin I; Ang.(1-9);  
 KW blood pressure; hypertension; congestive heart failure; atherosclerosis;  
 KW chronic heart failure; acute heart failure; myocardial infarction;  
 KW renal failure.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200018899-A2.  
 XX  
 PD 06-APR-2000.  
 XX  
 PF 29-SEP-1999; 99WO-US22976.  
 XX  
 PR 30-SEP-1998; 98US-0163648.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Acton LS, Robison KE, Hsieh FY;  
 XX  
 DR WPI; 2000-293140/25.  
 XX  
 PT Isolated nucleic acid encoding angiotensin converting enzyme-2 (ACE-2)  
 PT polypeptide useful for detecting an ACE-2 therapeutic for treating  
 PT hypertension, congestive heart failure, myocardial infarction,  
 PT atherosclerosis and renal failure -  
 XX  
 PS Disclosure; Fig 8; 138pp; English.  
 XX  
 CC AAY84563-68 represent angiotensin I conversion products. The  
 CC specification describes a human angiotensin converting enzyme-2 (ACE-2).  
 CC ACE-2 is expressed predominantly in kidneys and testis. The sequence of  
 CC the full length ACE-2 cDNA was determined from a clone obtained from a  
 CC cDNA library prepared from mRNA of a human heart of a subject who had  
 CC congestive heart failure. ACE-2 has significant sequence homologies with  
 CC ACE enzymes, and has also been shown to hydrolyse angiotensin I into  
 CC Ang.(1-9). The ACE-2 therapeutics are used to treat blood pressure  
 CC related diseases and conditions, such as hypertension, congestive heart  
 CC failure, chronic heart failure, acute heart failure, myocardial  
 CC infarction, atherosclerosis and renal failure.  
 XX  
 SQ Sequence 5 AA;

Query Match 100.0%; Score 26; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
 |||||  
 Db 1 drvyI 5

Search completed: February 26, 2002, 08:16:39  
 Job time: 748 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 26, 2002, 08:13:06 ; Search time 12.46 Seconds  
(without alignments)  
9.030 Million cell updates/sec

Title: US-09-658-315-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
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3: /cgn2\_5/ptodata/2/iaa/6A\_COMB.pep.\*  
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5: /cgn2\_5/ptodata/2/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_5/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	5	2 US-08-465-775-9	Sequence 9, Appli
2	26	100.0	5	3 US-09-208-337-9	Sequence 9, Appli
3	26	100.0	5	3 US-08-990-664-10	Sequence 10, Appli
4	26	100.0	5	4 US-09-373-962-9	Sequence 9, Appli
5	26	100.0	5	4 US-09-245-680-9	Sequence 9, Appli
6	26	100.0	5	4 US-09-198-806C-9	Sequence 9, Appli
7	26	100.0	5	4 US-09-352-191-9	Sequence 9, Appli
8	26	100.0	6	2 US-08-465-775-8	Sequence 8, Appli
9	26	100.0	6	3 US-09-208-337-8	Sequence 8, Appli
10	26	100.0	6	3 US-08-990-664-9	Sequence 8, Appli
11	26	100.0	6	4 US-09-373-962-8	Sequence 8, Appli
12	26	100.0	6	4 US-09-245-680-8	Sequence 8, Appli
13	26	100.0	6	4 US-09-198-806C-8	Sequence 8, Appli
14	26	100.0	6	4 US-09-352-191-8	Sequence 8, Appli
15	26	100.0	7	2 US-08-465-775-4	Sequence 8, Appli
16	26	100.0	7	3 US-09-208-337-4	Sequence 4, Appli
17	26	100.0	7	3 US-08-990-664-5	Sequence 5, Appli
18	26	100.0	7	4 US-09-373-962-4	Sequence 4, Appli
19	26	100.0	7	4 US-09-245-680-4	Sequence 4, Appli
20	26	100.0	7	4 US-09-198-806C-4	Sequence 4, Appli
21	26	100.0	7	4 US-09-352-191-4	Sequence 4, Appli
22	26	100.0	7	6 5451571-4	Patent No. 5451571
23	26	100.0	8	1 US-07-858-842-2	Sequence 2, Appli
24	26	100.0	8	1 US-08-021-839A-3	Sequence 3, Appli
25	26	100.0	8	1 US-08-184-935-2	Sequence 2, Appli
26	26	100.0	8	1 US-08-212-433A-29	Sequence 29, Appli
27	26	100.0	8	1 US-08-185-448-8	Sequence 8, Appli

Sequence 1, Appli  
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Sequence 20, Appli  
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Sequence 1, Appli  
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Sequence 3, Appli  
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Sequence 2, Appli  
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Sequence 3, Appli  
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Sequence 29, Appli  
Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-465-775-9  
; Sequence 9, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizegere, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-465-775-9

Query Match 100.0%; Score 26; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
Db 1 DRVYI 5

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RESULT 2
US-09-208-337-9
; Sequence 9, Application US/09208337
; Patent No. 6096709
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: Gere, dizerega
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,337
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,775
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: 08/337,781
; FILING DATE: 14-NOV-1994
; APPLICATION NUMBER: 08/126,368
; FILING DATE: 24-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC010.001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 949-760-0404
; TELEFAX: 949-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
US-09-208-337-9

Query Match 100.0%; Score 26; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 3
US-08-990-664-10
; Sequence 10, Application US/08990664
; Patent No. 6110895
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING
; TITLE OF INVENTION: IN SKIN GRAFTS
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
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; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/990,664
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/028,310
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: USC012.001A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-990-664-10

Query Match 100.0%; Score 26; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 4
US-09-373-962-9
; Sequence 9, Application US/09373962
; Patent No. 6177407
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue
; FILE REFERENCE: 98364A
; CURRENT APPLICATION NUMBER: US/09/373,962
; CURRENT FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-373-962-9

Query Match 100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5
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; TITLE OF INVENTION: Growth and Repair
; FILE REFERENCE: 98365B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-352-191-9

Query Match      100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 8
US-08-465-775-8
; Sequence 8, Application US/08465775
; Patent No. 5955430
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dizerega, Gere S.
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o Robbins, Berliner & Carson
; STREET: 201 No. 5955430th Figueroa Street #500
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,775
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-360
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-775-8

Query Match      100.0%; Score 26; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

; TITLE OF INVENTION: Growth and Repair
; FILE REFERENCE: 98365B
; CURRENT APPLICATION NUMBER: US/09/352,191
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-352-191-9

Query Match      100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 6
US-09-198-806C-9
; Sequence 9, Application US/09198806C
; Patent No. 6248587
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation
; FILE REFERENCE: 97,017-F1
; CURRENT APPLICATION NUMBER: US/09/198,806C
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-5)
US-09-198-806C-9

Query Match      100.0%; Score 26; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 7
US-09-352-191-9
; Sequence 9, Application US/09352191
; Patent No. 6258778
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue
```

RESULT 9  
US-09-208-337-8  
; Sequence 8, Application US/09208337  
; Patent No. 6096709  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: Gere, dizerega  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS  
; TITLE OF INVENTION: AND ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/208,337  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/465,775  
; FILING DATE: 06-JUN-1995  
; APPLICATION NUMBER: 08/337,781  
; FILING DATE: 14-NOV-1994  
; APPLICATION NUMBER: 08/126,368  
; FILING DATE: 24-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC010.001CP2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 949-760-0404  
; TELEFAX: 949-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-208-337-8

Query Match 100.0%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
Db 1 DRVYI 5

RESULT 10  
US-08-990-664-9  
; Sequence 9, Application US/08990664  
; Patent No. 6110895  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: METHOD OF PROMOTING HEALING  
; TITLE OF INVENTION: IN SKIN GRAFTS  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 620 Newport Center Drive 16th Floor  
; CITY: Newport Beach  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92660  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/990,664  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/028,310  
; FILING DATE: 16-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Altman, Daniel E  
; REGISTRATION NUMBER: 34,115  
; REFERENCE/DOCKET NUMBER: USC012.001A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 714-760-0404  
; TELEFAX: 714-760-9502  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-990-664-9

Query Match 100.0%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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Db 1 DRVYI 5

RESULT 11  
US-09-373-962-8  
; Sequence 8, Application US/09373962  
; Patent No. 6177407  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Methods to Increase Blood Flow to Ischemic Tissue  
; FILE REFERENCE: 98364A  
; CURRENT APPLICATION NUMBER: US/09/373,962  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-373-962-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||

Db 1 DRVVI 5

## RESULT 12

US-09-245-680-8  
; Sequence 8, Application US/09245680B  
; Patent No. 6239109  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method of Promoting Erythropoiesis  
; FILE REFERENCE: 98009B  
; CURRENT APPLICATION NUMBER: US/09/245,680B  
; CURRENT FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-245-680-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVVI 5

|||||

Db 1 DRVVI 5

## RESULT 13

US-09-198-806C-8  
; Sequence 8, Application US/09198806C  
; Patent No. 6248587  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere  
; TITLE OF INVENTION: Method for Promoting Mesenchymal Stem  
; TITLE OF INVENTION: and Lineage-Specific Cell Proliferation  
; FILE REFERENCE: 97,017-F1  
; CURRENT APPLICATION NUMBER: US/09/198,806C  
; CURRENT FILING DATE: 1998-11-24  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-198-806C-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVVI 5

|||||

Db 1 DRVVI 5

## RESULT 14

US-09-352-191-8  
; Sequence 8, Application US/09352191  
; Patent No. 6258778  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen  
; APPLICANT: dizerega, Gere

Query Match 100.0%; Score 26; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVVI 5

|||||

Db 1 DRVVI 5

; TITLE OF INVENTION: Methods for Accelerating Bone and Connective Tissue  
; TITLE OF INVENTION: Growth and Repair  
; FILE REFERENCE: 98365B  
; CURRENT APPLICATION NUMBER: US/09/352,191  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: AII (1-6)  
US-09-352-191-8

Query Match 100.0%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVVI 5

|||||

Db 1 DRVVI 5

## RESULT 15

US-08-465-775-4  
; Sequence 4, Application US/08465775  
; Patent No. 5955430  
; GENERAL INFORMATION:  
; APPLICANT: Rodgers, Kathleen E.  
; APPLICANT: dizerega, Gere S.  
; TITLE OF INVENTION: USE OF ANGIOTENSIN II FRAGMENTS AND  
; TITLE OF INVENTION: ANALOGS THEREOF IN TISSUE REPAIR  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o Robbins, Berliner & Carson  
; STREET: 201 No. 5955430th Figueroa Street #500  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90012  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,775  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spitals, John P.  
; REGISTRATION NUMBER: 29,215  
; REFERENCE/DOCKET NUMBER: 1920-360  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 977-1001  
; TELEFAX: (213) 977-1003  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-465-775-4

Db 1 DRVYI 5

Search completed: February 26, 2002, 08:16:58  
Job time: 232 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:14:01 ; Search time 12.81 Seconds  
(without alignments)  
29.732 Million cell updates/sec

Title: US-09-658-315-9  
Perfect score: 26  
Sequence: 1 DRVYI 5  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68.\*  
1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	10	2 S65432	angiotensin I - ho
2	26	100.0	14	2 A01250	angiotensin precu
3	26	100.0	15	2 A60834	angiotensin I prec
4	26	100.0	115	2 A48793	glycosylation-inhi
5	26	100.0	115	2 I52370	macrophage migrati
6	26	100.0	115	2 A44499	macrophage migrati
7	26	100.0	115	2 C47274	migration inhibito
8	26	100.0	167	2 F83686	hypothetical prote
9	26	100.0	195	1 B69441	conserved hypotet
10	26	100.0	238	2 E70337	ABC transporter -
11	26	100.0	248	2 T44932	3-oxoacyl-[acyl-ca
12	26	100.0	312	2 T00992	hypothetical prote
13	26	100.0	409	1 G69000	molybdenum cofacto
14	26	100.0	476	1 JC2318	angiotensin precu
15	26	100.0	477	1 ANRT	angiotensin precu
16	26	100.0	477	1 A29978	angiotensin precu
17	26	100.0	485	1 ANHU	angiotensin precu
18	26	100.0	509	2 T06300	hypothetical prote
19	26	100.0	518	2 B64449	hypothetical prote
20	26	100.0	540	2 S72233	2-isopropylmalate
21	26	100.0	575	1 HNNZS2	transcription fact
22	26	100.0	575	1 HNNZSH	hemagglutinin-neu
23	26	100.0	575	2 S12135	hemagglutinin-neu
24	26	100.0	576	1 HNNZS	hemagglutinin-neu
25	26	100.0	581	1 A37913	serine/threonine-s
26	26	100.0	614	2 T43121	hypothetical prote
27	26	100.0	644	2 G64938	hypothetical prote
28	26	100.0	644	2 F82145	conserved hypotet
29	26	100.0	644	2 H85788	hypothetical prote

30	26	100.0	661	2 C83843	hypothetical prote
31	26	100.0	676	1 WMBEX6	UL6 protein - huma
32	26	100.0	688	2 A44306	polyphosphate kina
33	26	100.0	688	2 G85893	polyphosphate kina
34	26	100.0	739	2 I40715	malate synthase (E
35	26	100.0	749	2 S77175	senesory transducti
36	26	100.0	778	2 T44761	probable preprotei
37	26	100.0	808	2 F70720	probable transloca
38	26	100.0	838	2 T40203	conserved hypotet
39	26	100.0	1062	2 H83966	carbamoyl-phosphat
40	26	100.0	1071	2 F39845	carbamoyl-phosphat
41	26	100.0	1076	2 A69409	carbamoyl-phosphat
42	26	100.0	1238	2 A64596	hypothetical prote
43	26	100.0	1296	1 BTCLAB	bontulixysin (EC 3
44	26	100.0	1296	2 I40645	botulinum neurotox
45	26	100.0	3194	2 D71917	toxin-like outer m

ALIGNMENTS

RESULT 1

S65432  
angiotensin I - horn fly (fragment)  
C:Species: Haematobia irritans (horn fly)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S65432  
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willad  
Eur. J. Biochem. 237, 414-423, 1996  
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the di  
A:Reference number: S65431; MUID:96215437  
A:Accession: S65432  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <WIJ>  
A>Note: the source is designated as Haematobia irritans exigua

Query Match 100.0%; Score 26; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 1 DRVYI 5

RESULT 2

A01250  
angiotensin precursor - horse (fragment)  
C:Species: Equus caballus (domestic horse)  
C:Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 20-Mar-1998  
C:Accession: A92775; A01250  
R:Skeggss Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.  
J. Exp. Med. 106, 439-453, 1957  
A:Reference number: A92775  
A:Accession: A92775  
A:Molecule type: protein  
A:Residues: 1-14 <SKE>  
C:Superfamily: antithrombin III  
C:Keywords: blood pressure control; hormone; vasoconstrictor  
F:1-10/Product: angiotensin II #status experimental <AN1>  
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 100.0%; Score 26; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 1 DRVYI 5

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RESULT 3
A60834
angiotensin I precursor - dog (fragment)
N;Alternate names: angiotensinogen I
N;Contains: angiotensin I
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Mar-1998
C;Accession: A60834
R;Oliver, J.A.
Hypertension 11, 21-27, 1988
A;Title: Purification and partial characterization of canine angiotensinogen.
A;Reference number: A60834; MUID:88113996
A;Accession: A60834
A;Molecule type: protein
A;Residues: 1-15 <OLI>
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; plasma
F;1-10/Product: angiotensin I #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 1 DRVYI 5

RESULT 4
A48793
glycosylation-inhibiting factor - human
N;Alternate names: macrophage migration inhibitory 12.7K protein; sarcolectin
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jul-2000
C;Accession: A48793; A33838; A47274; S34300; S33277
R;Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993
A;Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-in
A;Reference number: A48793; MUID:94052102
A;Accession: A48793
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-115 <MIK>
A;Cross-references: GB:L10612; NID:g402701; PIDN:AAA35892.1; PID:g402702
R;Paralkar, V.; Wistow, G.
Genomics 19, 48-51, 1994
A;Title: Cloning the human gene for macrophage migration inhibitory factor (MIF).
A;Reference number: A49612; MUID:94245178
A;Accession: A49612
A;Molecule type: DNA
A;Residues: 1-115 <PAR>
A;Cross-references: GB:L19686; NID:g307284; PIDN:AAA21814.1; PID:g307285
R;Weiser, W.Y.; Temple, P.A.; Witek-Glannotti, J.S.; Remold, H.G.; Clark, S.C.; David, J
Proc. Natl. Acad. Sci. U.S.A. 86, 7522-7526, 1989
A;Title: Molecular cloning of a cDNA encoding a human macrophage migration inhibitory fa
A;Reference number: A33838; MUID:90017510
A;Accession: A33838
A;Molecule type: mRNA
A;Residues: 1-105, S', 107-115 <WEI>
A;Cross-references: GB:M25639; NID:g188555; PIDN:AAA36315.1; PID:g188556
A;Experimental source: activated T cells
R;Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993
A;Title: A macrophage migration inhibitory factor is expressed in the differentiating ce
A;Reference number: A47274; MUID:93165679
A;Accession: A47274
A;Molecule type: mRNA
A;Residues: 10-115 <WIS>
A;Cross-references: GB:M95775; NID:g187180; PIDN:AAA36179.1; PID:g187181
A;Experimental source: fetal lens
A;Note: sequence extracted from NCBI backbone (NCBIN:124868, NCBIP:124871)

R;Bucala, R.; Mitchell, R.A.; Bernhagen, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34300
A;Accession: S34300
A;Molecule type: mRNA
A;Residues: 1-115 <BUC>
A;Cross-references: EMBL:Z23063; NID:g312333; PIDN:CAA80598.1; PID:g312334
R;Zeng, F.Y.; Weiser, W.Y.; Kratzin, H.; Stahl, B.; Karas, M.; Gabius, H.J.
Arch. Biochem. Biophys. 303, 74-80, 1993
A;Title: The major binding protein of the interferon antagonist sarcolectin in huma
A;Reference number: S33277; MUID:93256574
A;Accession: S33277
A;Molecule type: protein
A;Residues: 3-24 <ZEN>
A;Experimental source: placenta
A;Note: there is no signal sequence; the mature protein starts with residue 3
C;Genetics:
A;Gene: GDB:MIF
A;Cross-references: GDB:L38402; OMIM:153620
A;Map position: 22q11.2-22q11.2
A;Introns: 36/3; 94/2
A;Note: appears to be a single copy gene (see reference A49612)
C;Superfamily: bovine glycosylation-inhibiting factor
F;3-115/Product: macrophage migration inhibitory factor #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 93 DRVYI 97

RESULT 5
I52370
macrophage migration inhibitory factor MIF [similarity] - rat
C;Species: Rattus sp. (rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I52370
R;Sakai, M.; Nishihira, J.; Hibiya, Y.; Koyama, Y.; Nishi, S.
Biochem. Mol. Biol. Int. 33, 439-446, 1994
A;Title: Glutathione binding rat liver 13k protein is the homologue of the macrophr
A;Reference number: I52370; MUID:95038523
A;Accession: I52370
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-115 <RES>
A;Cross-references: GB:S73424; NID:g663139; PIDN:AAB32392.1; PID:g663140
C;Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 93 DRVYI 97

RESULT 6
A44499
macrophage migration inhibitory factor DER6 - mouse
N;Alternate names: glycosylation-inhibiting factor; migration inhibitory factor, 10k
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: A44499; S34299; B47274; I49691; S38325; I56259
R;Lanahan, A.; Williams, J.B.; Sanders, L.K.; Nathans, D.
Mol. Cell. Biol. 12, 3919-3929, 1992
A;Title: Growth factor-induced delayed early response genes.
A;Reference number: A44499; MUID:92375060

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A:Accession: A44499  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-115 <LAN>  
A:Experimental source: BALB/c 3T3 cells  
A>Note: sequence extracted from NCBI backbone (NCBIP:1111643)  
R:Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.; Tracey, K.J.; Manogue, K.; Voelter, W.; submitted to the EMBL Data Library, June 1993  
A:Reference number: S34299  
A:Accession: S34299  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-115 <BER>  
A:Cross-references: EMBL:223048; NID:g312220; PIDN:CAA80583.1; PID:g312221  
R:Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993  
A:Title: A macrophage migration inhibitory factor is expressed in the differentiating cells  
A:Reference number: A47274; MUID:93165679  
A:Accession: B47274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 6-115 <WIS>  
A:Cross-references: GB:L07607; NID:g191490; PIDN:AAA37111.1; PID:g191491  
A:Experimental source: lens  
A>Note: sequence extracted from NCBI backbone (NCBIN:124869, NCBIP:124872)  
R:Mikayama, T.; Nakano, T.; Gomi, H.; Nakagawa, Y.; Liu, Y.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10056-10060, 1993  
A:Title: Molecular cloning and functional expression of a cDNA encoding glycosylation-inhibiting factor  
A:Reference number: A48793; MUID:94052102  
A:Accession: I49691  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-115 <RES>  
A:Cross-references: GB:L10613; NID:g402716; PIDN:AAA37693.1; PID:g402717  
R:Bernhagen, J.; Calandra, T.; Mitchell, R.A.; Martin, S.B.; Tracey, K.J.; Voelter, W.; Nature 365, 756-759, 1993  
A:Title: MIF is a pituitary-derived cytokine that potentiates lethal endotoxaemia.  
A:Reference number: S38325; MUID:94019845  
A:Accession: S38325  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 2-28 <BE2>  
A:Cross-references: EMBL:223048  
R:Mitchell, R.; Bacher, M.; Bernhagen, J.; Pushkarskaya, T.; Seldin, M.F.; Bucala, R. J. Immunol. 154, 3863-3870, 1995  
A:Title: Cloning and characterization of the gene for mouse macrophage migration inhibitory factor  
A:Reference number: I56259; MUID:95221891  
A:Accession: I56259  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-115 <RE2>  
A:Cross-references: GB:L39357; NID:g790847; PIDN:AAA74321.1; PID:g790848  
C:Genetics:  
A:Gene: Mif  
A:Introns: 36/3; 94/2  
C:Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
Db 93 DRVYI 97

RESULT 7  
C47274  
migration inhibitory factor, 10K - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000  
C:Accession: C47274

R:Wistow, G.J.; Shaughnessy, M.P.; Lee, D.C.; Hodin, J.; Zelenka, P.S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1272-1275, 1993  
A:Title: A macrophage migration inhibitory factor is expressed in the differentiating cells  
A:Reference number: A47274; MUID:93165679  
A:Accession: C47274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-115 <WIS>  
A:Cross-references: GB:M95776; NID:g212257; PIDN:AAA48939.1; PID:g212258  
A:Experimental source: embryo, lens  
A>Note: sequence extracted from NCBI backbone (NCBIN:124870, NCBIP:124873)  
C:Superfamily: bovine glycosylation-inhibiting factor

Query Match 100.0%; Score 26; DB 2; Length 115;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
Db 93 DRVYI 97

RESULT 8  
F83686  
hypothetical protein BH0294 [imported] - Bacillus halodurans (strain C-125)  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 31-Dec-2000  
C:Accession: F83686  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans  
A:Reference number: A83650; MUID:20263314  
A:Accession: F83686  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-167 <STO>  
A:Cross-references: GB:AP001508; GB:BA000004; NID:g10172890; PIDN:BA04013.1; GSPDP  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0294

Query Match 100.0%; Score 26; DB 2; Length 167;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
|||||  
Db 61 DRVYI 65

RESULT 9  
B69441  
conserved hypothetical protein AFL531 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: B69441  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D. ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997  
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Syke Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon Pyrococcus furiosus  
A:Reference number: A69250; MUID:98049343  
A:Accession: B69441  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-195 <KLE>  
A:Cross-references: GB:AE000997; GB:AE000782; NID:g2689320; PIDN:AAB89717.1; PID:g2.  
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0038

Query Match 100.0%; Score 26; DB 1; Length 195;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 68 DRVYI 72

RESULT 10

E70337

ABC transporter - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 02-Feb-2001

C:Accession: E70337

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi-

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: E70337

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-238 <AOFP>

A:Cross-references: GB:AE000689; NID:g2983082; PIDN:AAC06695.1; PID:g2983089; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: abcT7

C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

C:Keywords: ATP; nucleotide binding; P-loop

F:17-210/Domain: ATP-binding cassette homology <ABC>

F:34-41/Region: nucleotide-binding motif A (P-loop)

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 238;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 202 DRVYI 206

RESULT 11

T44932

3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [Imported] - Agrobacterium tum

C:Species: Agrobacterium tumefaciens

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T44932

R:Kim, K.S.; Farrand, S.K.

J. Bacteriol. 178, 3275-3284, 1996

A:Title: Ti plasmid-encoded genes responsible for catabolism of the crown gall opine man

by the plant tumor.

A:Reference number: 222872; MUID:96236046

A:Accession: T44932

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-248 <KTM>

A:Cross-references: EMBL:U19620; NID:g797330; PIDN:AAB07783.1; PID:g797334

A:Experimental source: strain 15955

C:Genetics:

A:Gene: mocc

A:Genome: plasmid pT15955

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 248;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 221 DRVYI 225

RESULT 12

T00992

hypothetical protein At2g26590 [Imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T9J22.26

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 23-Mar-2001

C:Accession: T00992; D84662

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.;

submitted to the EMBL Data Library, April 1998

A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.

A:Reference number: Z14161

A:Accession: T00992

A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-312 <ROU>

A:Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739383

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Vente

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: D84662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-312 <STO>

A:Cross-references: GB:AE002093; NID:g2739383; PIDN:AAC14506.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g26590; T9J22.26

A:Map position: 2

A:Introns: 11/3; 42/3; 62/3; 100/3; 124/2; 169/2; 210/1; 241/3; 267/3; 286/1

Query Match

Best Local Similarity 100.0%; Score 26; DB 2; Length 312;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5

Db 81 DRVYI 85

RESULT 13

G69000

molybdenum cofactor biosynthesis protein MoeA - Methanobacterium thermoautotrophicum

C:Species: Methanobacterium thermoautotrophicum

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000

C:Accession: G69000

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, J.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan

ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: f

A:Reference number: A69000; MUID:98037514

A:Accession: G69000

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-409 <MTH>

A:Cross-references: GB:AE000873; GB:AE000666; NID:g2622101; PIDN:AAB85499.1; PID:g26;

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1003

A:Start codon: TTG

C:Superfamily: molybdenum cofactor biosynthesis protein moeA-2

Query Match

Best Local Similarity 100.0%; Score 26; DB 1; Length 409;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

|||||

Db 131 DRVYI 135

#### RESULT 14

JC2318

angiotensin precursor - sheep

N;Alternate names: angiotensinogen

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000

C;Accession: JC2318; A25406

R;Ngase, M.; Suzuki, F.; Fukamizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura

BioSci. Biotechnol. Biochem. 59, 1884-1885, 1994

A;Title: Sequencing and expression of sheep angiotensinogen cDNA.

A;Reference number: JC2318; MUID:95072318

A;Accession: JC2318

A;Molecule type: mRNA

A;Residues: 1-476 <NAG>

A;Cross-references: DDBJ:D17520; NID:g575593; PIDN:BAA04470.1; PID:g1197183

A;Experimental source: liver

A;Note: the authors translated the codon TTC for residue 465 as Leu

R;Fennley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.

Eur. J. Biochem. 154, 597-601, 1986

A;Title: Purification and characterization of ovine angiotensinogen.

A;Reference number: A25406; MUID:86136099

A;Accession: A25406

A;Molecule type: protein

A;Residues: 25-37, X, 39 <PER>

C;Superfamily: antithrombin III

C;Keywords: blood pressure control; glycoprotein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;24-476/Product: angiotensinogen #status predicted <MPT>

F;25-34/Product: angiotensin #status predicted <MAT>

F;295,362/Binding site: carbonylrate (Asn) (covalent) #status predicted

• Query Match

Best Local Similarity 100.0%; Score 26; DB 1; Length 476;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

|||||

Db 25 DRVYI 29

#### RESULT 15

ANRT

angiotensin precursor - rat

N;Contains: angiotensin I; angiotensin II; angiotensin III

C;Species: Rattus norvegicus (Norway rat)

C;Date: 13-Jun-1983 #sequence\_revision 13-Jun-1983 #text\_change 18-Jun-1999

C;Accession: A93945; A90456; A01251

R;Ohkubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.

Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983

A;Title: Cloning and sequenc analysis of cDNA for rat angiotensinogen.

A;Reference number: A93945; MUID:83169849

A;Accession: A93945

A;Molecule type: mRNA

A;Residues: 1-477 <OHK>

A;Cross-references: GB:L00094; GB:J00704; NID:g202912; PIDN:AAA98779.1; PID:g202914

R;Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.

Biochemistry 20, 7010-7015, 1981

A;Title: Rat angiotensinogen and Des(angiotensinI)angiotensinogen: purification, charact

A;Reference number: A90456; MUID:82091819

A;Accession: A90456

A;Molecule type: protein

A;Residues: 25-41 <BOU>

C;Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted in

e I (angiotensin-converting enzyme), primarily in the lungs.

C;Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and ang

sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I  
C;Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma  
ung.

C;Superfamily: antithrombin III

C;Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-477/Product: angiotensinogen #status predicted <MPT>

F;25-34/Product: angiotensin I #status experimental <PPL>

F;25-32/Product: angiotensin II #status experimental <PP2>

F;26-32/Product: angiotensin III #status experimental <PP3>

F;295,319/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match

100.0%; Score 26; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5

|||||

Db 25 DRVYI 29

Search completed: February 26, 2002, 08:17:18

Job time: 197 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 26, 2002, 08:16:16 ; Search time 10.14 Seconds  
(without alignments)  
18.079 Million cell updates/sec

Title: US-09-658-315-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
2	26	100.0	14	1 ANG2_HORSE	P01016 equus cabal
3	26	100.0	114	1 MIF_CHICK	Q02960 gallus gall
4	26	100.0	114	1 MIF_HUMAN	P14174 homo sapien
5	26	100.0	114	1 MIF_MOUSE	P34884 mus muscucu
6	26	100.0	114	1 MIF_RAT	P30904 rattus norv
7	26	100.0	436	1 TBX6_HUMAN	O95947 homo sapien
8	26	100.0	476	1 ANG2_SHEEP	P20757 ovis aries
9	26	100.0	477	1 ANG2_MOUSE	P11859 mus muscucu
10	26	100.0	477	1 ANG2_RAT	P01015 rattus norv
11	26	100.0	485	1 ANG2_HUMAN	P01019 homo sapien
12	26	100.0	518	1 YB95_METJA	Q58595 methanococc
13	26	100.0	540	1 TBX6_MOUSE	P70327 mus muscucu
14	26	100.0	575	1 HEMA_SENDS	P27562 sendai viru
15	26	100.0	575	1 HEMA_SENDF	P19758 sendai viru
16	26	100.0	575	1 HEMA_SENDJ	P06863 sendai viru
17	26	100.0	575	1 HEMA_SENDZ	P04853 sendai viru
18	26	100.0	576	1 HEMA_SENDH	P03425 sendai viru
19	26	100.0	581	1 MIK1_SCHPO	P30290 schizosacch
20	26	100.0	644	1 YEAG_ECOLI	P77391 escherichia
21	26	100.0	676	1 UL06_HSV11	P10190 herpes simp
22	26	100.0	687	1 PPK_ECOLI	P28688 escherichia
23	26	100.0	687	1 MAS2_CORGL	O86090 salmonella
24	26	100.0	738	1 SEA2_MYCLE	P42450 corynebacte
25	26	100.0	778	1 SEA2_MYCLE	O32922 mycobacteri
26	26	100.0	808	1 SEA2_MYCTU	O50612 mycobacteri
27	26	100.0	1071	1 CARB_BACSU	P25994 bacillus su
28	26	100.0	1295	1 BXA_CLOBO	P10845 clostridium
29	25	96.2	10	1 ANG1_BOTJA	Q10581 bothrops ja
30	25	96.2	10	1 ANG1_BOVIN	P01017 bos taurus
31	25	96.2	10	1 ANG1_CHICK	P01018 gallus gall
32	25	96.2	114	1 MIF_BOVIN	P80177 bos taurus
33	25	96.2	114	1 MIF_MERUN	O55052 meriones un

34	25	96.2	178	1	BDH_BOVIN	Q02337 bos taurus
35	25	96.2	272	1	PK1_NPVAC	P41415 autographa
36	25	96.2	311	1	NFE2_RHIME	Q52994 rhizobium m
37	25	96.2	446	1	GGAA_BACSU	P46917 bacillus su
38	25	96.2	465	1	YCL4_KLEPN	Q48460 klebsiella
39	25	96.2	488	1	GAL7_LACHE	Q00054 lactobacill
40	25	96.2	511	1	EGO_ECOLI	P77257 escherichia
41	25	96.2	539	1	PRIS_METJA	Q58175 methanococc
42	25	96.2	572	1	HEMA_P13B	P06167 bovine para
43	25	96.2	574	1	CDAS_THETB	P29964 thermoanaer
44	25	96.2	583	1	SECD_TREPA	O83425 treponema p
45	25	96.2	588	1	YO6B_CAEEL	P34602 caenorhabdi

ALIGNMENTS

RESULT 1						
ANG2_BOTJA						
ID	ANG2_BOTJA	STANDARD;	PRT;	8 AA.		
AC	Q10582;					
DT	01-OCT-1996 (Rel. 34, Created)					
DT	01-OCT-1996 (Rel. 34, Last sequence update)					
DT	15-DEC-1998 (Rel. 37, Last annotation update)					
DE	ANGIOTENSIN-LIKE PEPTIDE II (FRAGMENT).					
OS	Bothrops jararaca (Jararaca).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;					
OC	Viperidae; Crotalinae; Bothrops.					
OX	NCBI_TaxID=8724;					
RN	[1]					
RP	SEQUENCE.					
RC	TISSUE=Plasma;					
RX	MDLINE=96208932; PubMed=8829801;					
RA	Borghesi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;					
RT	"Isolation and identification of angiotensin-like peptides from the					
RL	plasma of the snake Bothrops jararaca."					
CC	-I- Biochem. Physiol. 113B:467-473(1996).					
DR	InterPro: IPR000215; Serpin.					
DR	PROSITE: PS00284; SERPIN: PARTIAL.					
KW	Vasoconstrictor; Plasma; Serpin.					
FT	NON_TER 8					
SQ	SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;					
Query Match	100.0%;	Score 26;	DB 1;	Length 8;		
Best Local Similarity	100.0%;	Pred. No. 1e+05;				
Matches	5; Conservative	0; Mismatches	0; Indels	0; Gaps	0;	
QY	1 DRVYI 5					
Db	1 DRVYI 5					
RESULT 2						
ANGT_HORSE						
ID	ANGT_HORSE	STANDARD;	PRT;	14 AA.		
AC	P01016;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DT	20-AUG-2001 (Rel. 40, Last annotation update)					
DE	ANGIOTENSINOGEN [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II] (FRAGMENT).					
GN	SERPINA8 OR AGT.					
OS	Equus caballus (Horse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.					
OX	NCBI_TaxID=9796;					
RN	[1]					
RP	SEQUENCE.					
RA	Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;					
RT	"The preparation, purification, and amino acid sequence of a					
	polypeptide renin substrate."					

```

RL J. Exp. Med. 106:439-453(1957).
CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
CC BALANCE OF BODY FLUIDS.
CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR PIR; A01250;
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 8 ANGIOTENSIN II.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
DB 1 |||||
1 DRVYI 5

RESULT 3
MIF_CHICK STANDARD; PRT; 114 AA.
AC Q02960;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPIRUVATE
DE TAUTOMERASE).
GN MIF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RA "A macrophage migration inhibitory factor is expressed in the
RT differentiating cells of the eye lens.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M95776; AAA48939.1; -.
DR PIR; C47274; C47274.
DR HSP; P14174; LGIF.
DR InterPro; IPR001398; MIF.
DR Pfam; PF01187; MIF; 1.
DR PROSITE; PS01158; MIF; 1.
KW Isomerase; Macrophage; Inflammatory response; Cytokine.
FT ACT_SITE 1 1 CATALYTIC BASE (BY SIMILARITY).

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FT INLT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12353 MW; A55222D00E6D05CF CRC64;

Query Match 100.0%; Score 26; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
DB 92 DRVYI 96
|||||

RESULT 4
MIF_HUMAN STANDARD; PRT; 114 AA.
AC P14174;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPIRUVATE
DE TAUTOMERASE) (GLYCOSYLATION-INHIBITING FACTOR) (GIF).
GN MIF OR MMIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90017510; PubMed=2552447;
RA Weiser W.Y., Temple P.A., Witek-Giannotti J.S., Remold H.G.,
RA Clark S.C., David J.R.;
RT "Molecular cloning of a cDNA encoding a human macrophage migration
RT inhibitory factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7522-7526(1989).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245178; PubMed=8188240;
RA Paralkar V., Wistow G.J.;
RT "Cloning the human gene for macrophage migration inhibitory factor
RT (MIF).";
RL Genomics 19:48-51(1994).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94052102; PubMed=8234256;
RA Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C.,
RA Iwamatsu A., Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;
RT "Molecular cloning and functional expression of a cDNA encoding
RT glycosylation-inhibiting factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).
[4]
RP SEQUENCE OF 9-114 FROM N.A.
RC TISSUE=Lens;
RX MEDLINE=93165679; PubMed=7679497;
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RA "A macrophage migration inhibitory factor is expressed in the
RT differentiating cells of the eye lens.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
[5]
RP SEQUENCE OF 1-10.
RC TISSUE=Liver;
RX MEDLINE=93162045; PubMed=1286669;
RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA Appel R.D., Hughes G.J.;
RT "Human liver protein map: a reference database established by
RT microsequencing and gel comparison.";
RL Electrophoresis 13:992-1001(1992).
[6]
RP SEQUENCE OF 2-23.
RX MEDLINE=93256574; PubMed=7683862;
RA Zeng F.Y., Weiser W.Y., Kratzin H., Stahl B., Karas M., Gabius H.J.;
RT "The major binding protein of the interferon antagonist sarcolectin

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in human placenta is a macrophage migration inhibitory factor.";  
 Arch. Biochem. Biophys. 303:74-80(1993).  
 [7]  
 RX MEDLINE=96338096; PubMed=8766818;  
 RA Sugimoto H., Suzuki M., Nakagawa A., Tanaka I., Nishihira J.;  
 RT "Crystal structure of macrophage migration inhibitory factor from  
 human lymphocyte at 2.1-A resolution.";  
 FEBS Lett. 389:145-148(1996).  
 [8]  
 RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).  
 RA MEDLINE=96181524; PubMed=8610159;  
 RA Kato Y., Muto T., Tomura T., Tsumura H., Watarai H., Mikayama T.,  
 RA Ishizaka K., Kuroki R.;  
 RT "The crystal structure of human glycosylation-inhibiting factor is a  
 trimeric barrel with three 6-stranded beta-sheets.";  
 Proc. Natl. Acad. Sci. U.S.A. 93:3007-3010(1996).  
 [9]  
 RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).  
 RA MEDLINE=96224259; PubMed=8643551;  
 RA Sun H.W., Bernhagen J., Bucala R., Lolis E.;  
 RT "Crystal structure at 2.6-A resolution of human macrophage migration  
 inhibitory factor.";  
 Proc. Natl. Acad. Sci. U.S.A. 93:5191-5196(1996).  
 [10]  
 RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RA MEDLINE=99282199; PubMed=10353846;  
 RA Lubetsky J.B., Swope M., Dealwis C., Blake P., Lolis E.;  
 RT "Pro-1 of macrophage migration inhibitory factor functions as a  
 catalytic base in the phenylpyruvate tautomerase activity.";  
 Biochemistry 38:7346-7354(1999).  
 CC -1- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A  
 CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN  
 CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- DISEASE: MIF ACTIVITY HAS BEEN DETECTED IN LEUKOCYTE CULTURE  
 CC SUPERNATANTS OF MICE DURING ALLOGRAFT REJECTION, IN THE SYNOVIA  
 CC OF PATIENTS WITH RHEUMATOID POLYARTHRITIS, AND IN A VARIETY OF  
 CC CHRONIC INFLAMMATORY LOC.  
 CC -1- SIMILARITY: BELONGS TO THE MIF FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Z23063; CAA80598.1; -;  
 DR EMBL; M25639; AAA36315.1; -;  
 DR EMBL; M95775; AAA36179.1; -;  
 DR EMBL; L10612; AAA35892.1; -;  
 DR EMBL; L19686; AAA21814.1; -;  
 DR PIR; A33838; A33838.  
 DR PIR; S33277; S33277.  
 DR PDB; 1GIF; 12-MAR-97.  
 DR PDB; 1MIF; 07-DEC-96.  
 DR PDB; 1P1G; 07-JUN-99.  
 DR PDB; 1CGG; 07-JUN-99.  
 DR PDB; 1CA7; 30-JUN-99.  
 DR SWISS-2DPAGE; P14174; HUMAN.  
 DR MIM; 153620; -;  
 DR InterPro: IPR001398; MIF.  
 DR Pfam; PF01187; MIF; 1.  
 DR PROSITE; PS01158; MIF; 1.  
 KW isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.  
 FT INIT\_MET 0 0  
 FT ACT\_SITE 1 1 CATALYTIC BASE.  
 FT CONFLICT 105 105 N -> S (IN REF. 1).  
 FT SEQUENCE 114 AA; 12345 MW; 4BDS25232B3F3069 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DRVYI 5  
 Db 92 DRVYI 96  
 |||||  
 RESULT 5  
 MIF\_MOUSE  
 ID MIR\_MOUSE STANDARD; PRT; 114 AA.  
 AC P34884;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPIRUVATE  
 DE TAUTOMERASE) (DELAYED EARLY RESPONSE PROTEIN 6) (DER6) (GLYCOSYLATION-  
 DE INHIBITING FACTOR).  
 GN MIF.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.  
 RC TISSUE-Pituitary;  
 RX MEDLINE=94019845; PubMed=8413654;  
 RA Bernhagen J., Calandra T., Mitchell R.A., Martin S.B.,  
 RA Tracey K.J., Voelker W., Manogue K.R., Cerami A., Bucala R.;  
 RT "MIF is a pituitary-derived cytokine that potentiates lethal  
 RT endotoxaemia.";  
 RN Nature 365:756-759(1993).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=92375060; PubMed=1508193;  
 RA Lanahan A., Williams J.B., Sanders L.K., Nathans D.;  
 RT "Growth factor-induced delayed early response genes.";  
 RN Mol. Cell. Biol. 12:3919-3929(1992).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94052102; PubMed=8234256;  
 RA Mikayama T., Nakano T., Gomi H., Nakagawa Y., Liu Y.C., Iwamatsu A.,  
 RA Weiser W.Y., Ishizaka K., Sato M., Ishii Y.;  
 RT "Molecular cloning and functional expression of a cDNA encoding  
 RT glycosylation-inhibiting factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:10056-10060(1993).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=95221891; PubMed=7706726;  
 RA Mitchell R., Bacher M., Bernhagen J., Pushkarskaya T., Seldin M.F.,  
 RA Bucala R.;  
 RT "Cloning and characterization of the gene for mouse macrophage  
 RT migration inhibitory factor (MIF).";  
 RL J. Immunol. 154:3863-3870(1995).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=96047325; PubMed=7558021;  
 RA Bozza M., Kolakowski L.F. Jr., Jenkins N.A., Gilbert D.J.,  
 RA Copeland N.G., David J.R., Gerard C.;  
 RT "Structural characterization and chromosomal location of the mouse  
 RT macrophage migration inhibitory factor gene and pseudogenes.";  
 RL Genomics 27:412-419(1995).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV;  
 RX MEDLINE=96047324; PubMed=7558020;  
 RA Kozak C.A., Adamson M.C., Buckler C.E., Segovia L., Paralkar V.,  
 RA Wistow G.;  
 RT "Genomic cloning of mouse MIF (macrophage inhibitory factor) and

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RT genetic mapping of the human and mouse expressed gene and nine mouse
RL pseudogenes."
RN Genomics 27:405-411(1995).
RP [7]
RX SEQUENCE OF 5-114 FROM N.A.
RC TISSUE=Lens;
RA MEDLINE=93165679; PubMed=7679497;
RA Wistow G.J., Shaughnessy M., Lee D.C., Hodin J., Zelenka P.S.;
RT "A macrophage migration inhibitory factor is expressed in the
RL differentiating cells of the eye lens.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1272-1275(1993).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=93303983; PubMed=10360941;
RA Taylor A.B., Johnson W.H. Jr., Czerwinski R.M., Li H.S., Hackert M.L.,
RA Whitman C.P.;
RT "Crystal structure of macrophage migration inhibitory factor
RT complexed with (E)-2-fluoro-p-hydroxycinnamate at 1.8 A resolution:
RT implications for enzymatic catalysis and inhibition.";
RL Biochemistry 38:7444-7452(1999).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.00 ANGSTROMS).
RX MEDLINE=20393856; PubMed=10933783;
RA Stamps S.L., Taylor A.B., Wang S.C., Hackert M.L., Whitman C.P.;
RA "Mechanism of the phenylpyruvate tautomerase activity of macrophage
RT migration inhibitory factor: properties of the PIG, PIA, Y95F, and
RT N97A mutants.";
RL Biochemistry 39:9671-9678(2000).
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC -----
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CC -----
CC EMBL; Z23048; CAA80583.1; -
CC EMBL; U19825; AAA91637.1; -
CC EMBL; L10613; AAA37893.1; -
CC EMBL; U20156; AAA91638.1; -
CC EMBL; L39357; AAA74321.1; -
CC EMBL; L07607; AAA37111.1; -
CC PIR; S34299; S34299.
CC PIR; A44499; A44499.
CC PDB; IMFF; 11-AUG-00.
CC PDB; IMFI; 22-JUN-99.
CC MGD; MGI:96982; Mif.
CC InterPro; IPR001398; MIF.
CC Pfam; PF01187; MIF; 1.
CC PROSITE; PS01158; MIF; 1.
CC Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 1
FT CATALYTIC BASE.
SQ SEQUENCE 114 AA; 12373 MW; 8FD2339CF0792F9E CRC64;

Query Match 100.08; Score 26; DB 1; Length 114;
Best Local Similarity 100.08; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
      |||||
Db 92 DRVYI 96

RESULT 6
MIF_RAT

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ID MIF_RAT STANDARD; PRT; 114 AA.
AC P30904;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MACROPHAGE MIGRATION INHIBITORY FACTOR (MIF) (PHENYLPIRUVATE
DE TAUTOMERASE) (GLUTATHIONE-BINDING 13 KDA PROTEIN).
GN MIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95038523; PubMed=7951062;
RA Sakai M., Nishihira J., Hibiyu Y., Koyama Y., Nishi S.;
RT "Glutathione binding rat liver 13k protein is the homologue of the
RT macrophage migration inhibitory factor.";
RL Biochem. Mol. Biol. Int. 33:439-446(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lens;
RA Wen Y., Li G., Bekhor I.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=PVG/C;
RA Sleeman M.A., Huckle J.W., Robinson M., Jahoda C.A.B.,
RA Reynolds A.J., Whitehouse C.J.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-25.
RX MEDLINE=93063370; PubMed=1436109;
RT Blocki F.A., Schlievert P.M., Wackett L.P.;
RT "Rat liver protein linking chemical and immunological detoxification
RT systems";
RL Nature 360:269-270(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC TISSUE=Liver;
RX MEDLINE=96186248; PubMed=8605628;
RA Suzuki M., Sugimoto H., Nakagawa A., Tanaka I., Nishihira J.,
RA Sakai M.;
RT "Crystal structure of the macrophage migration inhibitory factor from
RT rat liver.";
RL Nat. Struct. Biol. 3:259-266(1996).
CC -!- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
CC ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
CC HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF ORGANS
CC INCLUDING BRAIN, SPLEEN, LIVER, MUSCLE AND KIDNEY.
CC -!- SIMILARITY: BELONGS TO THE MIF FAMILY.
CC -----
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CC -----
CC EMBL; S73424; AAB32392.1; -
CC EMBL; U20999; AAA62644.1; -
CC EMBL; U62326; AAB04024.1; -
CC PDB; IFIM; 11-JUL-96.
CC InterPro; IPR001398; MIF.
CC Pfam; PF01187; MIF; 1.
CC PROSITE; PS01158; MIF; 1.
CC Isomerase; Macrophage; Inflammatory response; Cytokine; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 1
FT CATALYTIC BASE (BY SIMILARITY).

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FT CONFLICT 50 50 S -> R (IN REF. 2).
SQ SEQUENCE 114 AA; 12346 MW; 9E33C39CF064329E CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 1; Length 114;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 92 DRVYI 96

RESULT 7
TBX6_HUMAN
ID TBX6_HUMAN STANDARD; PRT; 436 AA.
AC O95947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE T-BOX TRANSCRIPTION FACTOR TBX6 (T-BOX PROTEIN 6).
GN TBX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99134303; PubMed=9933572;
RA Papapetrou C., Putt W., Fox M., Edwards Y.H.;
RT "The human TBX6 gene: Cloning and assignment to chromosome 16p11.2.";
RL Genomics 55:238-241(1999).
[2]
RP SEQUENCE OF 135-272 FROM N.A.
RX MEDLINE=99107806; PubMed=9888994;
RA Yi C.-H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,
RT "Identification, mapping and phylogenomic analysis of four new human
members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19.";
RL Genomics 55:10-20(1999).
CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN
DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF
PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).
CC -1- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL
TISSUE, INTERVERTEBRAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT
TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A
SECOND PHASE IN SOME ADULT TISSUES.
CC -1- SIMILARITY: CONTAINS A T-BOX DOMAIN.
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EMBL; AJ007989; CAA07812.1; -.
DR EMBL; AJ010279; CAB37938.1; -.
DR MIM; 602427; -.
DR InterPro; IPR001699; T-box.
DR Pfam; PF00907; T-box; 1.
DR PRINTS; PR00937; TBOX.
DR PRINTS; PR00938; BRACHYURY.
DR SMART; SM00425; TBOX; 1.
DR PROSITE; PS01283; TBOX_1; 1.
DR PROSITE; PS01284; TBOX_2; 1.
DR PROSITE; PS0252; TBOX_3; 1.
KW Transcription regulation; DNA-binding; Nuclear protein;

TBX6_HUMAN
ID ANGT_SHEEP STANDARD; PRT; 476 AA.
AC P20757;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].
GN SERPINA8 OR AGT.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95072318; PubMed=7765514;
RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
RA Murakami K., Nakamura Y.;
RT "Sequencing and expression of sheep angiotensinogen cDNA.";
RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
[2]
RP SEQUENCE OF 25-39.
RX MEDLINE=8613609; PubMed=3081342;
RA Farnley R.T., John M., Niall H.D., Coghlan J.P.;
RT "Purification and characterization of ovine angiotensinogen.";
RL Eur. J. Biochem. 154:597-601(1986).
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
BALANCE OF BODY FLUIDS.
CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
-----
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or send an email to license@isb-sib.ch).
```

FT CARBOHYD 295 295 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 26; DB 1; Length 476;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 DB 25 DRVYI 29  
 |||||

RESULT 9  
 ANGT\_MOUSE STANDARD; PRT; 477 AA.  
 AC P11859;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].  
 GN SERPINA8 OR AGT.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88284703; PubMed=3397061;  
 RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;  
 RL "Molecular cloning of the mouse angiotensinogen gene.";  
 CC Genomics 2:240-248(1988).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF045887; AAC01765.1;  
 DR EMBL; AF045886; AAC01765.1; JOINED.  
 DR EMBL; AF045885; AAC01765.1; JOINED.  
 DR EMBL; AF045884; AAC01765.1; JOINED.  
 DR PIR; A29978; A29978.  
 DR MGD; MGI:87963; Agt.  
 DR InterPro; IPR000227; Angiotensngn.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR PRINTS; PR00654; ANGIOTENSNGN.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 477 ANGIOTENSINOGEN.  
 FT PEPTIDE 25 34 ANGIOTENSIN I.  
 FT PEPTIDE 25 32 ANGIOTENSIN II.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 401 401 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 477 AA; 51990 MW; A877F4029F338607 CRC64;

Query Match  
 100.0%; Score 26; DB 1; Length 477;

Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 DB 25 DRVYI 29  
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RESULT 10  
 ANGT\_RAT STANDARD; PRT; 477 AA.  
 ID ANGT\_RAT  
 AC P01015;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].  
 GN SERPINA8 OR AGT.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WISTAR.  
 RX MEDLINE=83169849; PubMed=6572971;  
 RA Ohkubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,  
 RA Nakanishi S.;  
 RL "Cloning and sequence analysis of cDNA for rat angiotensinogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).  
 RN [2]  
 RP SEQUENCE OF 25-34.  
 RX MEDLINE=73060322; PubMed=4344907;  
 RA Nakayama T., Nakajima T., Sokabe H.;  
 RT "Comparative studies on angiotensins. II. Structure of rat  
 RT angiotensin and its identification by DNS-method.";  
 RL Chem. Pharm. Bull. 20:1579-1581(1972).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; L00094; AAA98779.1;  
 DR EMBL; L00091; AAA98779.1; JOINED.  
 DR EMBL; L00092; AAA98779.1; JOINED.  
 DR EMBL; L00093; AAA98779.1; JOINED.  
 DR PIR; A01251; ANRT.  
 DR InterPro; IPR000227; Angiotensngn.  
 DR InterPro; IPR000215; Serpin.  
 DR Pfam; PF00079; serpin; 1.  
 DR PRINTS; PR00654; ANGIOTENSNGN.  
 DR SMART; SM00093; SERPIN; 1.  
 DR PROSITE; PS00284; SERPIN; FALSE\_NEG.  
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.  
 FT SIGNAL 1 24  
 FT CHAIN 25 477 ANGIOTENSINOGEN.  
 FT PEPTIDE 25 34 ANGIOTENSIN I.  
 FT PEPTIDE 25 32 ANGIOTENSIN II.  
 FT CARBOHYD 295 295 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 319 319 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 477 AA; 51981 MW; 689051A5788D693D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
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DB 25 DRVYI 29

RESULT 11  
ANGT\_HUMAN  
ID ANGT\_HUMAN STANDARD; PRT; 485 AA.  
AC P01019; Q16358; Q16359;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE ANGIOTENSINOGEN PRECURSOR [CONTAINS: ANGIOTENSIN I; ANGIOTENSIN II].  
GN SERPINB8 OR AGT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89170129; PubMed=2924688;  
RA Gaillard I., Clausen E., Corvol P.;  
RT "Structure of human angiotensinogen gene.";  
RL DNA 8:87-99(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85000455; PubMed=6089875;  
RA Kageyama R., Onkubo H., Nakanishi S.;  
RT "Primary structure of human preangiotensinogen deduced from the  
RT cloned cDNA sequence.";  
RL Biochemistry 23:3603-3609(1984).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90237063; PubMed=1692023;  
RA Fukamizu A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,  
RA Murakami K.;  
RT "Structure and expression of the human angiotensinogen gene.  
RT Identification of a unique and highly active promoter.";  
RL J. Biol. Chem. 265:7576-7582(1990).  
RN [4]  
RP SEQUENCE OF 1-338 FROM N.A.  
RX MEDLINE=87244745; PubMed=2885106;  
RA Kunapuli S.P., Kumar A.;  
RT "Molecular cloning of human angiotensinogen cDNA and evidence for the  
RT presence of its mRNA in rat heart.";  
RL Circ. Res. 60:786-790(1987).  
RN [5]  
RP SEQUENCE OF 34-43.  
RX MEDLINE=69014170; PubMed=4300938;  
RA Arakawa K., Minohara A., Yamada J., Nakamura M.;  
RT "Enzymatic degradation and electrophoresis of human angiotensin I.";  
RL Biochim. Biophys. Acta 168:106-112(1968).  
RN [6]  
RP STRUCTURE BY NMR OF ANGIOTENSIN II.  
RX MEDLINE=98151281; PubMed=9492317;  
RA Carpenter K.A., Wilkes B.C., Schiller P.W.;  
RT "The octapeptide angiotensin II adopts a well-defined structure in a  
RT phospholipid environment.";  
RL Eur. J. Biochem. 251:448-453(1998).  
RN [7]  
RP VARIANTS MET-207; THR-268 AND CYS-281.  
RX MEDLINE=93008239; PubMed=1394429;  
RA Jeunenaiire X., Soubrier F., Kotelevtsev Y.V., Lifton R.P.,  
RA Williams C.S., Charu A., Hunt S.C., Hopkins P.N., Williams R.R.,  
RA Lalouel J.-M., Corvol P.;  
RT "Molecular basis of human hypertension: role of angiotensinogen.";  
RL Cell 71:169-180(1992).  
RN [8]

RP VARIANT THR-268  
RX MEDLINE=93291876; PubMed=8513325;  
RA Ward K., Hata A., Jeunenaiire X., Helin C., Nelson L., Namikawa C.,  
RA Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,  
RA Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;  
RT "A molecular variant of angiotensinogen associated with  
RT preeclampsia.";  
RL Nat. Genet. 4:59-61(1993).  
RN [9]  
RP VARIANTS ILE-242; ARG-244 AND CYS-281.  
RX MEDLINE=95331754; PubMed=7607642;  
RA Hixson J.E., Powers P.K.;  
RT "Detection and characterization of new mutations in the human  
RT angiotensinogen gene (AGT).";  
RL Hum. Genet. 96:110-112(1995).  
CC -|- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
CC CLEAVES ANGIOTENSIN I. FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
CC BALANCE OF BODY FLUIDS.  
CC -|- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.  
CC -|- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO  
CC ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION  
CC (PIH) (PREECLAMPSIA).  
CC -|- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
CC -|- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.  
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CC  
CC EMBL; K02215; AAA51731.1; -;  
DR EMBL; M24689; AAA51679.1; -;  
DR EMBL; M24686; AAA51679.1; JOINED.  
DR EMBL; M24687; AAA51679.1; JOINED.  
DR EMBL; M24688; AAA51679.1; JOINED.  
DR EMBL; M24689; AAA51679.1; JOINED.  
DR EMBL; X15324; CAA33385.1; -;  
DR EMBL; X15325; CAA33385.1; JOINED.  
DR EMBL; X15326; CAA33385.1; JOINED.  
DR EMBL; X15327; CAA33385.1; JOINED.  
DR EMBL; M69110; AAA52282.1; -;  
DR EMBL; S78529; AAD14287.1; -;  
DR EMBL; S78530; AAD14288.1; -;  
DR PIR; A01249; ANHU.  
DR PIR; A31362; A31362.  
DR PIR; A35203; A35203.  
DR SWISS-2DPAGE; P01019; HUMAN.  
DR MIM; 106150; -;  
DR InterPro; IPR000227; Angiotensn.  
DR InterPro; IPR000215; Serpin.  
DR Pfam; PF00079; serpin; 1.  
DR PRINTS; PR00654; ANGIOTENSNGN.  
DR SMART; SM00093; SERPIN; 1.  
DR PROSITE; PS00284; SERPIN; 1.  
DR Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal;  
KW Disease mutation; Polymorphism.  
FT SIGNAL 1 33  
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FT PEPTIDE 34 43 ANGIOTENSIN I.  
FT PEPTIDE 34 41 ANGIOTENSIN II.  
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FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 304 304 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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FT /FTID=VAR\_007093.  
FT T-> I (IN HYPERTENSION).  
FT VARIANT 242 242  
FT /FTID=VAR\_007094.  
FT

FT VARIANT 244 244 L -> R (IN HYPERTENSION).  
 FT /FTID=VAR\_007095.  
 FT VARIANT 268 268 M -> T (IN HYPERTENSION).  
 FT /FTID=VAR\_007096.  
 FT VARIANT 281 281 Y -> C (IN HYPERTENSION).  
 FT /FTID=VAR\_007097.  
 FT CONFLICT 333 333 /FTID=VAR\_007097.  
 SQ SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD236E CRC64;

Query Match 100.0%; Score 26; DB 1; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYI 5  
 DB 34 DRVYI 38

RESULT 12  
 YB95\_METJA STANDARD; PRT; 518 AA.  
 AC O58595;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE PUTATIVE 2-ISOPROPYLMALATE/HOMOCITRATE SYNTHASE MJ1195 (EC 4.1.3.-).  
 GN MJ1195.  
 OS Methanococcus jannaschii.  
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;  
 CC Methanococcus.  
 OX NCBI\_TaxID=2190;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;  
 RX MEDLINE=96337999; PubMed=8688087;  
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,  
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,  
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,  
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii.";  
 RT Science 273:1058-1073(1996).  
 CC -1- SIMILARITY: BELONGS TO THE ALPHA-IPM SYNTHETASE / HOMOCITRATE  
 CC SYNTHASE FAMILY.

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EMBL; U67561; AAB99199.1; -.  
 TIGR; MJ1195; -.  
 DR InterPro: IPR002034; AIPM\_homocit\_synth.  
 DR InterPro: IPR000891; HMGL-like.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR PROSITE; PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1.  
 DR PROSITE; PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1.  
 KW Hypothetical protein; Lyase; Complete proteome.  
 SQ SEQUENCE 518 AA; 56620 MW; 604AB61B41E607A4 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 518;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYI 5  
 DB 22 DRVYI 26

RESULT 13  
 TBX6\_MOUSE STANDARD; PRT; 540 AA.  
 ID TBX6\_MOUSE  
 AC P70327;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE T-BOX TRANSCRIPTION FACTOR TBX6 (T-BOX PROTEIN 6).  
 GN TBX6.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=97032942; PubMed=8878690;  
 RA Agulnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,  
 RA Agulnik I., Bollag R.J., Papaioannou V.E., Silver L.M.;  
 RT "Evolution of mouse T-box genes by tandem duplication and cluster  
 dispersion.";  
 RT Genetics 144:249-254(1996).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Gastrula;  
 RX MEDLINE=97115702; PubMed=8954725;  
 RA Chapman D.L., Agulnik I., Hancock S., Silver L.M., Papaioannou V.E.;  
 RT "Tbx6, a mouse T-Box gene implicated in paraxial mesoderm formation at  
 gastrulation.";  
 RL Dev. Biol. 180:534-542(1996).  
 RN [3]  
 RP FUNCTION.

EMBL; U67561; AAB99199.1; -.  
 TIGR; MJ1195; -.  
 DR InterPro: IPR002034; AIPM\_homocit\_synth.  
 DR InterPro: IPR000891; HMGL-like.  
 DR Pfam; PF00682; HMGL-like; 1.  
 DR PROSITE; PS00815; AIPM\_HOMOCIT\_SYNTH\_1; 1.  
 DR PROSITE; PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1.  
 KW Hypothetical protein; Lyase; Complete proteome.  
 SQ SEQUENCE 518 AA; 56620 MW; 604AB61B41E607A4 CRC64;

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EMBL; U57331; AAC53110.1; -.  
 HSSP; P24781; IXHR.  
 DR MGD; MGI:102539; Tbx6.  
 DR InterPro: IPR001699; T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS50252; TBOX\_3; 1.

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EMBL; U57331; AAC53110.1; -.  
 HSSP; P24781; IXHR.  
 DR MGD; MGI:102539; Tbx6.  
 DR InterPro: IPR001699; T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01283; TBOX\_1; 1.  
 DR PROSITE; PS01264; TBOX\_2; 1.  
 DR PROSITE; PS50252; TBOX\_3; 1.

KW Transcription regulation; DNA-binding; Nuclear protein;  
 KW Developmental protein.  
 FT DOMAIN 61 64 POLY-ALA.  
 FT DOMAIN 79 82 POLY-PRO.  
 FT DNA\_BIND 100 273 T-BOX.  
 SQ SEQUENCE 540 AA; 58628 MW; BC834CE2745E8561 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 540;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 |||||

Db 170 DRVYI 174

RESULT 14  
 HEMA\_SENDS STANDARD; PRT; 575 AA.  
 AC P27562;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ-NEURAMINIDASE (EC 3.2.1.18).  
 GN HN.

OS Sendai virus (strain Z / host mutants).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.  
 OX NCBI\_TaxID=11192;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MUTANT TS-F1, AND MUTANT F1-R;  
 RX MEDLINE=90266486; PubMed=2161155;  
 RA Middleton V., Tashiro M., Thai T., Oh J., Seymour J., Pritzer E.,  
 RA Klenk H.D., Rott R., Seto J.T.;  
 RT "Nucleotide sequence analyses of the genes encoding the HN, M, NP, P,  
 RT and L proteins of two host range mutants of Sendai virus.";  
 RL Virology 176:656-657(1990).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=MUTANT F1-R / T-5 REVERTANT;  
 RX MEDLINE=91335752; PubMed=1651590;  
 RA Tashiro M., James I., Karri S., Wahn K., Tobita K., Klenk H.D.,  
 RA Rott R., Seto J.T.;  
 RT "Pneumotropic revertants derived from a pantropic mutant, F1-R, of  
 RT Sendai virus.";  
 RL Virology 184:227-234(1991).

CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-(2->3)-, ALPHA-(2->6)-,  
 CC ALPHA-(2->8)-GLYCOSIDIC LINKAGES OF TERMINAL SIALIC RESIDUES IN  
 CC OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS, COLOMINIC ACID AND  
 CC SYNTHETIC SUBSTRATES.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.

CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.

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DR EMBL; M30202; AAB06282.1; -;  
 DR EMBL; M30203; AAB06288.1; -;  
 DR EMBL; M30204; AAB06200.1; -;

DR EMBL; M69046; AAB06294.1; -;  
 DR InterPro; IPR000665; Hem-neuramndse.  
 DR Pfam; PF00423; HN; 1.  
 KW Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;  
 KW Transmembrane.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 60 POTENTIAL.  
 FT DOMAIN 61 575 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 499 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 511 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 575 AA; 63469 MW; 86EE95B73AD7EB2D CRC64;

Query Match 100.0%; Score 26; DB 1; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 67;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 |||||

Db 419 DRVYI 423

RESULT 15  
 HEMA\_SENDF STANDARD; PRT; 575 AA.  
 AC P19758;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE HEMAGGLUTININ-NEURAMINIDASE (EC 3.2.1.18).  
 GN HN.

OS Sendai virus (strain Fushimi).  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Paramyxovirus.  
 OX NCBI\_TaxID=11195;  
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91057133; PubMed=2173829;  
 RA Neubert W.J., Willenbrink W.;  
 RT "Cloning and sequencing of the HN gene of Sendai virus (strain  
 RT Fushimi).";  
 RL Nucleic Acids Res. 18:6427-6427(1990).

CC -1- FUNCTION: HEMAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VIRUS  
 CC TO CELL RECEPTORS AND FOR INITIATING INFECTION. NEURAMINIDASE  
 CC ACTIVITY HELPS THE EFFICIENT SPREAD OF THE VIRUS BY DISSOCIATING  
 CC THE MATURE VIRIONS FROM THE NEURAMINIC ACID CONTAINING  
 CC GLYCOPROTEINS.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF ALPHA-(2->3)-, ALPHA-(2->6)-,  
 CC ALPHA-(2->8)-GLYCOSIDIC LINKAGES OF TERMINAL SIALIC RESIDUES IN  
 CC OLIGOSACCHARIDES, GLYCOPROTEINS, GLYCOLIPIDS, COLOMINIC ACID AND  
 CC SYNTHETIC SUBSTRATES.

CC -1- SUBCELLULAR LOCATION: EXTERNAL, ANCHORED TO THE ENVELOPE BY ITS  
 CC N-TERMINAL HYDROPHOBIC SEQUENCE.

CC -1- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES HEMAGGLUTININ-  
 CC NEURAMINIDASE FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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DR EMBL; X56131; CAA39596.1; -;  
 DR PIR; S12135; S12135.  
 DR PIR; S12462; S12462.

DR InterPro; IPR000665; Hem-neuramndse.

DR Pfam; PF00423; HN; 1.

KW Hydrolase; Hemagglutinin; Envelope protein; Glycoprotein;

KW Transmembrane.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 36 60 POTENTIAL.  
FT DOMAIN 61 575 EXTRACELLULAR (POTENTIAL).  
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 575 AA; 63347 MW; 93FD0532F6147BF6 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 575;  
Best Local Similarity 100.0%; Pred. No. 67;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYI 5  
|||||  
Db 419 DRVYI 423

Search completed: February 26, 2002, 08:18:04  
Job time: 108 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: February 26, 2002, 08:15:41 ; Search time 22.88 Seconds  
(without alignments)  
31.965 Million cell updates/sec

Title: US-09-658-315-9  
Perfect score: 26  
Sequence: 1 DRVYI 5

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues 473505  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL\_17.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_unclassified.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	26	100.0	14	5	Q10757	Q10757 theromyzon
2	26	100.0	72	2	Q9R540	Q9r540 clostridium
3	26	100.0	87	8	Q9G9H0	Q9g9h0 eretmocerus
4	26	100.0	167	2	Q9KG21	Q9kg21 bacillus ha
5	26	100.0	173	12	Q88184	Q88184 san miguel
6	26	100.0	178	1	Q9HIS3	Q9his3 thermoplas
7	26	100.0	186	5	Q9W387	Q9w387 drosophila
8	26	100.0	195	1	Q28741	Q28741 archaeglob
9	26	100.0	238	2	O66729	O66729 aquifex aeo
10	26	100.0	248	2	Q44326	Q44326 agrobacteri
11	26	100.0	291	3	Q9C445	Q9c445 penicillium
12	26	100.0	291	4	Q9HBV1	Q9hbv1 homo sapien
13	26	100.0	291	11	Q9ES81	Q9es81 mus musculu
14	26	100.0	295	4	Q9HA44	Q9ha44 homo sapien
15	26	100.0	312	10	O48726	O48726 arabidopsis
16	26	100.0	321	5	Q9GNL3	Q9gnl3 drosophila
17	26	100.0	340	12	Q9DVM3	Q9dvm3 plutella xy
18	26	100.0	369	13	Q9IAE7	Q9iae7 pantodon bu
19	26	100.0	377	13	Q9IAG5	Q9iag5 gymnaarchus

20	26	100.0	408	10	Q9MA64	Q9ma64 arabidopsis
21	26	100.0	409	1	O27084	O27084 methanobact
22	26	100.0	461	11	Q9D2V0	Q9d2v0 mus musculu
23	26	100.0	485	6	Q9GLP7	Q9glp7 pan troglod
24	26	100.0	485	6	Q9GLP6	Q9glp6 gorilla gor
25	26	100.0	485	6	Q9GLN8	Q9gln8 pan troglod
26	26	100.0	486	6	Q9TS20	Q9ts20 callithrix
27	26	100.0	509	10	Q9T0L4	Q9t0l4 arabidopsis
28	26	100.0	575	12	O88413	O88413 sendai viru
29	26	100.0	614	2	O87250	O87250 lactococcus
30	26	100.0	644	2	Q9KQX5	Q9kqx5 vibrio chol
31	26	100.0	661	2	Q9KCM3	Q9kcm3 bacillus ha
32	26	100.0	749	2	P73687	P73687 synechocyst
33	26	100.0	798	2	Q9E2L3	Q9ezl3 mycobacteri
34	26	100.0	838	3	O94653	O94653 schizosacch
35	26	100.0	1047	1	Q9HK17	Q9hk17 thermoplas
36	26	100.0	1062	2	Q9K9V9	Q9k9v9 bacillus ha
37	26	100.0	1076	1	O28994	O28994 archaeglob
38	26	100.0	1238	2	O25330	O25330 helicobacte
39	26	100.0	1280	5	Q9V255	Q9v255 drosophila
40	26	100.0	1296	2	Q45894	Q45894 clostridium
41	26	100.0	1812	4	Q9ULL3	Q9ull3 homo sapien
42	26	100.0	2018	4	Q9NZM0	Q9nzm0 homo sapien
43	26	100.0	2048	4	Q9HBU3	Q9hbu3 homo sapien
44	26	100.0	2061	4	Q9NZM1	Q9nzm1 homo sapien
45	26	100.0	2433	12	O91464	O91464 aichi virus

ALIGNMENTS

RESULT 1  
Q10757  
ID Q10757 PRELIMINARY; PRT; 14 AA.  
AC Q10757;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE ANGIOSENSINOGEN (FRAGMENT)  
OS Theromyzon tessulatum (Leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudiniida; Hirudinea;  
OC Rhynchobdellida; Glossiphoniidae; Theromyzon.  
OX NCBI\_TaxID=13286;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95365039; PubMed=7637887;  
RA Laurent V., Bulet P., Salzet M.A.;  
RT "A comparison of the leech Theromyzon tessulatum angiotensin I-like  
RT molecule with forms of vertebrate angiotensinogens: a hormonal system  
RT conserved in the course of evolution.";  
RL Neurosci. Lett. 190:175-178(1995).  
RN [2]  
RP SEQUENCE OF 1-10.  
RC TISSUE=BRAIN;  
RX MEDLINE=96201949; PubMed=8612806;  
RA Laurent V., Salzet M.;  
RT "Metabolism of angiotensins by head membranes of the leech Theromyzon  
RT tessulatum.";  
RL FEBS Lett. 384:123-127(1996).  
CC -!- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.  
KW Glycoprotein; Serpin.  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DRVYI 5  
Db 1 DRVII 5

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RESULT 2
Q9R540
ID Q9R540 PRELIMINARY; PRT; 72 AA.
AC Q9R540;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE NEUROTOXIN HEAVY CHAIN 18 KDA FRAGMENT (FRAGMENT).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=94000342; PubMed=8397793;
RA Gimenez J.A., DasGupta B.R.;
RT "Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72,
RT 45, 42, and 18 kD fragments.";
RL J. Protein Chem. 12:351-363(1993).
DR HSSP; P10845; 38TA.
SQ SEQUENCE 72 AA; 8165 MW; B7A959576A615E18 CRC64;

Query Match 100.0%; Score 26; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db |||||
31 DRVYI 35

RESULT 3
Q9G9H0
ID Q9G9H0 PRELIMINARY; PRT; 87 AA.
AC Q9G9H0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CYTOCHROME OXIDASE II (FRAGMENT).
OS Eretmococcus mundus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apoecrita;
OC Chalcidoidea; Aphelinidae; Eretmococcus.
OX NCBI_TaxID=77302;
RN [1]
RP SEQUENCE FROM N.A.
RA De Barro P.J., Driver F., Naumann I.D., Clarke G.M., Curran J.;
RT "Descriptions of three species of Eretmocerus Haldeman (Hymenoptera:
RT Aphelinidae) parasitising Bemisia tabaci (Gennadius) (Hemiptera:
RT Aleyrodidae) and Trialeurodes vaporariorum (Westwood) (Hemiptera:
RT Aleyrodidae) in Australia based on morphological and molecular data.";
RL Aust. J. Entomol. 0:0-0(2000).
DR EMBL; AF275275; AAG25079.1; -.
DR InterPro; IPR001505; COX2.
DR Pfam; PF00116; COX2; 1.
DR PRINTS; PR01166; CYCOXIDASBII.
DR ProDom; PD000131; COX2; 1.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 87
SQ SEQUENCE 87 AA; 10387 MW; 43E205FB2E1C6FEC CRC64;

Query Match 100.0%; Score 26; DB 8; Length 87;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db |||||
```

```
Db 81 DRVYI 85

RESULT 4
Q9KG21
ID Q9KG21 PRELIMINARY; PRT; 167 AA.
AC Q9KG21;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BH0294 PROTEIN.
GN BH0294.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001508; BAB04013.1; -.
KW Complete proteome.
SQ SEQUENCE 167 AA; 19535 MW; 0C33F04D1A2E834D CRC64;

Query Match 100.0%; Score 26; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db |||||
61 DRVYI 65

RESULT 5
Q88184
ID Q88184 PRELIMINARY; PRT; 173 AA.
AC Q88184;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE RNA-DEPENDENT RNA POLYMERASE (FRAGMENT).
OS San Miguel sea lion virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Vesivirus.
OX NCBI_TaxID=11982;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SEROTYPE 5;
RX MEDLINE=95287505; PubMed=7769708;
RA Neill J.D., Meyer R.F., Seal B.S.;
RT "Genetic relatedness of the caliciviruses: San Miguel sea lion and
RT vesicular exanthema of swine viruses constitute a single genotype
RT within the Caliciviridae.";
RL J. Virol. 69:4484-4488(1995).
DR EMBL; U18731; AAA82219.1; -.
DR InterPro; IPR001643; CaliciCoat.
DR PRINTS; PR00918; CALICIVIRUSN.
DR RNA-directed RNA polymerase.
FT NON_TER 1
FT NON_TER 173
SQ SEQUENCE 173 AA; 19532 MW; 1830C8461CC21F7F CRC64;

Query Match 100.0%; Score 26; DB 12; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 DRVYI 5
Db 50 DRVYI 54

RESULT 6
Q9HIS3 PRELIMINARY; PRT; 178 AA.
ID Q9HIS3
AC Q9HIS3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PROBABLE 50S RIBOSOMAL PROTEIN L6.
GN TAL255.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmataceae;
OC Thermoplasma
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
DR EMBL: AL445067; CAC12379.1; -
DR InterPro: IPR000702; Ribosomal_L6.
DR Pfam: PF00347; Ribosomal_L6; 1.
DR ProDom: PD002236; Ribosomal_L6; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 178 AA; 19641 MW; 33B1312C268886A5 CRC64;

Query Match 100.0%; Score 26; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 134 DRVYI 138

RESULT 7
Q9W387 PRELIMINARY; PRT; 186 AA.
ID Q9W387
AC Q9W387
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CG12664 PROTEIN.
DE CG12664 OR CG12664.
GN LD14 OR CG12664.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Pterygota; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003446; AAF46447.1; -
DR FlyBase: FBgn0030090; ldl4.
SQ SEQUENCE 186 AA; 20461 MW; D2B4ED097ACA6420 CRC64;

Query Match 100.0%; Score 26; DB 5; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 110 DRVYI 114

RESULT 8
Q28741 PRELIMINARY; PRT; 195 AA.
ID Q28741
AC Q28741
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF1531.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J., Hickey E.K., Peterson J.D.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Kyrpides N.C.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Sutton G.G., Gill S.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).

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DR EMBL; AE000997; AAB89717.1; -.
DR TIGR; AF1531; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 195 AA; 23194 MW; C244F95420565E2C CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 1; Length 195;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 68 DRVYI 72

RESULT 9
O66729
ID O66729 PRELIMINARY; PRT; 238 AA.
AC O66729;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ABC TRANSPORTER.
GN ABC7 OR AQ_413.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RF "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC
CC TRANSPORTERS).
CC EMBL; AE000689; AAC06695.1; -.
DR InterPro; IPR003593; AAA.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR001687; ATP_GTP_A.
DR Pfam; PF00005; ABC_tran; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
KW ATP-binding; Complete proteome; Transport.
SQ SEQUENCE 238 AA; 26457 MW; 032A46CD90CEA8E5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 238;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 202 DRVYI 206

RESULT 10
Q44326
ID Q44326 PRELIMINARY; PRT; 248 AA.
AC Q44326;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MOCC PROTEIN.
GN MOCC.
OS Agrobacterium radiobacter.
OG Plasmid pTII5955.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=358;

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RN SEQUENCE FROM N.A.
RP STRAIN=15955;
RX MEDLINE=96236046; PubMed=8655509;
RA Kim K.S., Farrand S.K.;
RT "Ti plasmid-encoded genes responsible for catabolism of the crown gall
RT opine mannopine by Agrobacterium tumefaciens are homologs of the T-
RT region genes responsible for synthesis of this opine by the plant
RT tumor."
RL J. Bacteriol. 178:3275-3284(1996).
CC -1- SIMILARITY: TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR)
CC FAMILY.
DR EMBL; AF242881; AAB07783.1; -.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase; plasmid.
SQ SEQUENCE 248 AA; 26810 MW; 10B69239CDEBB68D CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 2; Length 248;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 221 DRVYI 225

RESULT 11
Q9C445
ID Q9C445 PRELIMINARY; PRT; 291 AA.
AC Q9C445;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PAXU.
GN PAXU.
OS Penicillium paxilli.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichoscomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=70109;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed-11169115;
RA Young C., McMillan L., Telfer E., Scott B.;
RT "Molecular cloning and genetic analysis of an indole-diterpene gene
RL Mol. Microbiol. 39:754-764(2001).
DR EMBL; AF279808; AAK11532.1; -.
SQ SEQUENCE 291 AA; 32954 MW; CFC35136FD40763E CRC64;

Query Match
Best Local Similarity 100.0%; Score 26; DB 3; Length 291;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5
Db 16 DRVYI 20

RESULT 12
Q9HBV1
ID Q9HBV1 PRELIMINARY; PRT; 291 AA.
AC Q9HBV1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE POPEYE PROTEIN 3.
GN POP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20341060; PubMed=10882522;  
 RA Andrew B., Hillemann T., Kessler-Ickson G., Schmitt-John T.,  
 RA Jockusch H., Arnold H.H., Brand T.;  
 RT "Isolation and characterization of the novel popeye gene family  
 RT expressed in skeletal muscle and heart."  
 RL Dev. Biol. 223:371-382(2000).  
 DR EMBL: AF204171; AAG23404.1; -;  
 SQ SEQUENCE 291 AA; 33810 MW; 49B6EF5DBC02DDC2 CRC64;

Query Match 100.0%; Score 26; DB 4; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 Db 248 DRVYI 252  
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RESULT 13  
 Q9ES81 PRELIMINARY; PRT; 291 AA.  
 ID Q9ES81  
 AC Q9ES81;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE POPEYE PROTEIN 3.  
 GN POP3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20341060; PubMed=10882522;  
 RA Andrew B., Hillemann T., Kessler-Ickson G., Schmitt-John T.,  
 RA Jockusch H., Arnold H.H., Brand T.;  
 RT "Isolation and characterization of the novel popeye gene family  
 RT expressed in skeletal muscle and heart."  
 RL Dev. Biol. 223:371-382(2000).  
 DR EMBL: AF204176; AAG23409.1; -;  
 DR MGD; MGI:1930153; POP3.  
 SQ SEQUENCE 291 AA; 33612 MW; 8AC6BFE107AEE12 CRC64;

Query Match 100.0%; Score 26; DB 11; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 Db 248 DRVYI 252  
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RESULT 14  
 Q9HA44 PRELIMINARY; PRT; 295 AA.  
 ID Q9HA44  
 AC Q9HA44;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE CDNA FLJ12268 FIS. CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS  
 DE TRANSCRIPTION FACTOR TBX6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=MAMMARY GLAND;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
 RA Nimoto Y., Iwayanagi T.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK022330; BAB14014.1; -;  
 DR InterPro; IPR001699; T-box.  
 DR Pfam; PF00907; T-box; 1.  
 DR PRINTS; PR00937; TBOX.  
 DR SMART; SM00425; TBOX; 1.  
 DR PROSITE; PS01264; TBOX 2; 1.  
 DR PROSITE; PS0252; TBOX 3; 1.  
 SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match 100.0%; Score 26; DB 4; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 Db 170 DRVYI 174  
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RESULT 15  
 O48726 PRELIMINARY; PRT; 312 AA.  
 ID O48726  
 AC O48726;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)  
 DE T9J22.26 PROTEIN.  
 GN T9J22.26.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, COLUMBIA;  
 RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C.,  
 RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,  
 RA Somerville C.R., Venter J.C.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC002505; AAC14506.1; -;  
 SQ SEQUENCE 312 AA; 34764 MW; 229F3B94EF849310 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 312;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYI 5  
 Db 81 DRVYI 85  
 |||||

Search completed: February 26, 2002, 08:17:48  
 Job time: 127 sec

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